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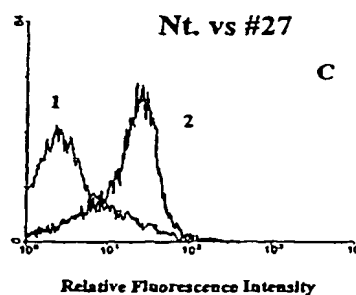
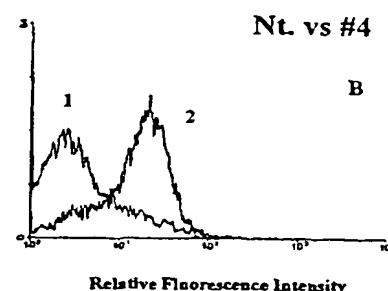
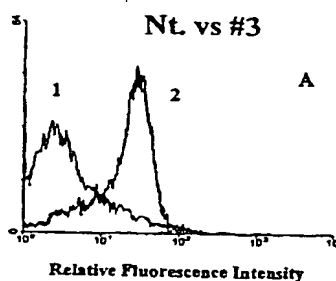
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(54) Title: **IL-9/IL-2 RECEPTOR-LIKE MOLECULES AND USES THEREOF**

(57) Abstract

Novel IL-9/IL-2 receptor-like polypeptides, proteins, and nucleic acids molecules are disclosed. In addition to isolated, full-length IL-9/IL-2 receptor-like proteins, the invention further provides isolated IL-9/IL-2 receptor-like fusion proteins, antigenic peptides, and anti-IL-9/IL-2 receptor-like antibodies. The invention also provides IL-9/IL-2 receptor-like nucleic acid molecules, recombinant expression vectors containing a nucleic acid molecule of the invention, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which IL-9/IL-2 receptor-like gene has been introduced or disrupted. Diagnostic, screening, and therapeutic methods utilizing compositions of the invention are also provided.



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IL-9/IL-2 RECEPTOR-LIKE MOLECULES AND USES THEREOF

FIELD OF THE INVENTION

The invention relates to novel IL-9/IL-2 receptor-like nucleic acid sequences and proteins. Also provided are vectors, host cells, and recombinant methods for making and using the novel molecules.

5

BACKGROUND OF THE INVENTION

Critical interactions among cells of the immune system are controlled by mediators called cytokines. A diverse group of cytokines that are structurally dissimilar and genetically unrelated have been identified. The cytokines serve as crucial intercellular-signaling molecules that are responsible for the multidirectional communication among immune and inflammatory cells engaged in host defense, repair, and restoration of homeostasis, as well as among other somatic cells in the connective tissues, skin, nervous system, and other organs. More particularly, this diverse group of intercellular-signaling proteins regulates local and systemic immune and inflammatory responses as well as wound healing, hematopoiesis, and many other biological processes. Each cytokine is secreted by particular cell types in response to a variety of stimuli and produces a characteristic constellation of effects on the growth, motility, differentiation, or function of its target cells. In fact, cytokines regulate one another's production and activities. Other types of biological mediators, such as corticosteroids and prostaglandins, have agonistic or antagonistic effects on cytokine activities.

Interleukin-2 (IL-2) is an autocrine and paracrine growth factor that is secreted by activated T lymphocytes. IL-2 is a critical immunoregulatory cytokine as it is essential for clonal T-cell proliferation, is involved in cytokine production, and influences the functional properties of B cells, macrophages, and NK cells. IL-2 enhances proliferation and antibody secretion by normal B cells. However, the concentration required for the B-cell response is two- to three-fold higher than

is required to obtain T-cell responses. Higher concentrations of IL-2 can also activate neutrophils. IL-2 exhibits a short half-life in the circulation. Thus, it generally acts only on the cell that secreted it or on cells in the immediate vicinity.

The IL-2 molecule is a 15,400 molecular weight polypeptide having 133 amino acids. The molecule is encoded by a gene on human chromosome 4. The encoded protein is composed of two α helices arranged to form hydrophobic planar faces around a very hydrophobic core.

The IL-2 receptor is not expressed in resting T cells but is induced to maximal levels within two or three days after the cells become activated. A decline in receptor expression occurs up to 6-10 days after activation. This transient nature of IL-2 receptor expression maintains the cyclical, self-limiting pattern of normal T-cell growth *in vivo*.

Interleukin-9 (IL-9) is a cytokine produced by activated Th2 cells upon stimulation with antigen. The cDNA sequence has been cloned. See, Wang *et al.* (1989) *Blood* 74:1880-1884. Both human and murine protein sequences contain 144 residues with a signal peptide of 18 amino acids. IL-9 expression seems to be mainly restricted to activated T cells.

IL-9 is capable of inducing the proliferation of mast cell lines, without the need for any additional growth factors. Besides this growth promoting activity, IL-9 may play a key role in mast cell differentiation by regulating the expression of mast cell proteases. IL-9 plays a role in Ig-mediated responses as suggested by the involvement of IL-9 in mast cell activation and proliferation, as well as the IL-9 production during parasite infections.

A variety of mouse hemopoietic cells, including T cells, mast cells, and macrophages, express high affinity receptors for IL-9. The murine receptor contains 468 amino acids including an extracellular domain, comprising 233 amino acids that shows the typical features of the hematopoietin receptor superfamily. The human IL-9 receptor cDNA encodes a 522 amino acid protein with 53% identity to the murine IL-9 receptor.

During the course of an immune response, T cells differentiate into Th phenotypes defined by their pattern of cytokine secretion and immunomodulatory properties (Abbas *et al.* (1996) *Nature* 383:787). Th cells are composed of at least two distinct subpopulations, termed Th1 and Th2 cell subpopulations (Mosmann *et*

al. (1989) *Ann. Rev. Immunol.* 7:145; Del Prete *et al.* (1991) *J. Clin. Invest.* 88:346; Wiernenga *et al.* (1990) *J. Immunol.* 144:4651; Yamamura *et al.* (1991) *Science* 254:277; Robinson *et al.* (1993) *J. Allergy Clin. Immunol.* 92:313). Th1 and Th2 cells appear to function as part of the different effector functions of the immune system (Mosmann *et al.* (1989) *Ann. Rev. Immunol.* 7:145). Specifically, Th1 cells direct the development of cell-mediated immunity, triggering phagocyte-mediated host defenses, and are associated with delayed hypersensitivity. Accordingly, infections with intracellular microbes tend to induce Th1-type responses. Th2 cells drive humoral immune responses, which are associated with, for example, defenses against certain helminthic parasites, and are involved in antibody and allergic responses.

Th1 cells secrete interleukin-2 (IL-2), interferon- γ (IFN- γ), and tumor necrosis factor- α (TNF- α). These cytokines enhance inflammatory cell-mediated responses and have a pathogenic role in the development of autoimmune disease. Th2 cells secrete interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-10 (IL-10), and interleukin-13 (IL-13). These cytokines suppress inflammatory responses while potentiating humoral immunity and control and reverse disease evolution (Scott *et al.* (1994) *Immunity* 1:73; Smith *et al.* (1998) *J. Immunol.* 160:4841; Abbas *et al.* (1996) *Nature* 383:787). The different type of cytokines released upon stimulation has been demonstrated to be central to disease evolution (Chu and Londei (1996) *J. Immunol.* 157:2685; Hsieh *et al.* (1993) *Science* 260:547).

The profile of the natural immune response, specifically cytokine production by natural killer cells or cells of basophil lineage, may determine the phenotype of the subsequent immune response. Therefore, methods are needed to regulate an immune response.

SUMMARY OF THE INVENTION

Isolated nucleic acid molecules corresponding to IL-9/IL-2 receptor-like nucleic acid sequences are provided. Additionally, amino acid sequences corresponding to the polynucleotides are encompassed. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in SEQ ID NO:2 and SEQ ID

NO:4 or the nucleotide sequences encoding the DNA sequence deposited in a bacterial host as ATCC Accession Number PTA-350, on July 14, 1999. Further provided are IL-9/IL-2 receptor-like polypeptides having an amino acid sequence encoded by a nucleic acid molecule described herein.

5 The present invention also provides vectors and host cells for recombinant expression of the nucleic acid molecules described herein, as well as methods of making such vectors and host cells and for using them for production of the polypeptides or peptides of the invention by recombinant techniques.

10 The IL-9/IL-2 receptor-like molecules of the present invention are useful for modulating the immune, inflammatory, and respiratory responses. The molecules are useful for the diagnosis and treatment of immune and respiratory disorders, particularly for the treatment and diagnosis of T-lymphocyte-related disorders, including, but not limited to, atopic conditions, such as asthma and allergy, including allergic rhinitis, psoriasis, the effects of pathogen infection,
15 chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, and graft versus host disease. Additionally, the molecules of the invention are useful as modulating agents in a variety of cellular processes including growth promoting activity, particularly the antigen-independent proliferation of T helper cell clones, and direct effects on normal hemopoietic progenitors, human T cells, B cells,
20 thymocytes, thymic lymphomas, and neuronal cell lines. Accordingly, in one aspect, this invention provides isolated nucleic acid molecules encoding IL-9/IL-2 receptor-like proteins or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like-encoding nucleic acids.

25 Another aspect of this invention features isolated or recombinant IL-9/IL-2 receptor-like proteins and polypeptides. Preferred IL-9/IL-2 receptor-like proteins and polypeptides possess at least one biological activity possessed by naturally occurring IL-9/IL-2 receptor-like proteins.

30 Variant nucleic acid molecules and polypeptides substantially homologous to the nucleotide and amino acid sequences set forth in the sequence listings are encompassed by the present invention. Additionally, fragments and substantially homologous fragments of the nucleotide and amino acid sequences are provided.

Antibodies and antibody fragments that selectively bind the IL-9/IL-2 receptor-like polypeptides and fragments are provided. Such antibodies are useful in detecting the IL-9/IL-2 receptor-like polypeptides as well as in regulating the T-cell immune response and cellular activity, particularly growth and proliferation.

5 In another aspect, the present invention provides a method for detecting the presence of IL-9/IL-2 receptor-like activity or expression in a biological sample by contacting the biological sample with an agent capable of detecting an indicator of IL-9/IL-2 receptor-like activity such that the presence of IL-9/IL-2 receptor-like activity is detected in the biological sample.

10 In yet another aspect, the invention provides a method for modulating IL-9/IL-2 receptor-like activity comprising contacting a cell with an agent that modulates (inhibits or stimulates) IL-9/IL-2 receptor-like activity or expression such that IL-9/IL-2 receptor-like activity or expression in the cell is modulated. In one embodiment, the agent is an antibody that specifically binds to IL-9/IL-2 receptor-like protein. In another embodiment, the agent modulates expression of
15 IL-9/IL-2 receptor-like protein by modulating transcription of an IL-9/IL-2 receptor-like gene, splicing of an IL-9/IL-2 receptor-like mRNA, or translation of an IL-9/IL-2 receptor-like mRNA. In yet another embodiment, the agent is a nucleic acid molecule having a nucleotide sequence that is antisense to the coding
20 strand of the IL-9/IL-2 receptor-like mRNA or the IL-9/IL-2 receptor-like gene.

In one embodiment, the methods of the present invention are used to treat a subject having a disorder characterized by aberrant IL-9/IL-2 receptor-like protein activity or nucleic acid expression by administering an agent that is an IL-9/IL-2 receptor-like modulator to the subject. In one embodiment, the IL-9/IL-2 receptor-
25 like modulator is an IL-9/IL-2 receptor-like protein. In another embodiment, the IL-9/IL-2 receptor-like modulator is an IL-9/IL-2 receptor-like nucleic acid molecule. In other embodiments, the IL-9/IL-2 receptor-like modulator is a peptide, peptidomimetic, or other small molecule.

The present invention also provides a diagnostic assay for identifying the
30 presence or absence of a genetic lesion or mutation characterized by at least one of the following: (1) aberrant modification or mutation of a gene encoding an IL-9/IL-2 receptor-like protein; (2) misregulation of a gene encoding an IL-9/IL-2 receptor-like protein; and (3) aberrant post-translational modification of an IL-

9/IL-2 receptor-like protein, wherein a wild-type form of the gene encodes a protein with an IL-9/IL-2 receptor-like activity.

In another aspect, the invention provides a method for identifying a compound that binds to or modulates the activity of an IL-9/IL-2 receptor-like protein. In general, such methods entail measuring a biological activity of an IL-9/IL-2 receptor-like protein in the presence and absence of a test compound and identifying those compounds that alter the activity of the IL-9/IL-2 receptor-like protein.

The invention also features methods for identifying a compound that modulates the expression of IL-9/IL-2 receptor-like genes by measuring the expression of the IL-9/IL-2 receptor-like sequences in the presence and absence of the compound.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the amino acid sequence alignment for the human and murine 16445 proteins (SEQ ID NO:2 and SEQ ID NO:4, respectively) encoded by human 16445 (SEQ ID NO:1) and its murine orthologue 16445 (SEQ ID NO:3) with the human IL-2 receptor beta chain (hIL-2Rb; SP Accession Number P14784; SEQ ID NO:5), murine IL-2 receptor beta chain (mIL-2Rb; SP Accession Number P16297; SEQ ID NO:6), human IL-9 receptor (hIL-9R; SP Accession Number Q01113; SEQ ID NO:7), and murine IL-9 receptor (mIL-9R; SP Accession Number Q01114; SEQ ID NO:8). The sequence alignment was generated using the Clustal method.

The human and murine 16445 protein sequences share approximately 64.4% identity as determined by pairwise alignment. The h16445 protein shares approximately 36.9% identity over a 130 amino acid overlap with the human IL-2 receptor beta chain, approximately 32.7% identity over a 110 amino acid overlap with the murine IL-2 receptor beta chain, approximately 29.7% identity over a 158 amino acid overlap with the human IL-9 receptor, and approximately 28.3%

identity over a 166 amino acid overlap with the murine IL-9 receptor, as determined by FASTA.

Figure 2 shows expression of h16445 in various tissues and cell types relative to expression in human hepatoma cell line Hep3B.

5 Figure 3A and 3B shows the effect of the ectopic expression of h16445 on cytokine-induced CAT expression in cells transfected with Type I cytokine receptors.

Figure 4 shows the increase in IL-9 induced CAT expression mediated by an IL-9R/h16445 cytoplasmic-domain receptor chimera.

10 Figure 5 shows FACs analysis screening of hybridoma supernatants (clone #s 4, 7, or 8) for binding to: (A) the GPI-linked h16445 extracellular domain expressed by HEK293 cells transiently transfected with a plasmid encoding amino acids 1-234 of the extracellular domain of h16445 plus a His tag and the C-terminal signal sequence from human placental alkaline phosphatase (GPI-linker signal), or (B) the h16445 extracellular domain expressed by HEK293 cells
15 transiently transfected with a plasmid encoding the full-length h16445 (B, C, and D). Relative fluorescence intensity exhibited by these transfected cells tagged with particular hybridoma supernatants (represented by peak 2 in panels A-D) is shown versus that exhibited by untransfected cells (represented by peak 1 in panels A-D),
20 which served as the control.

Figure 6 shows FACs analysis screening of h16445-specific hybridoma supernatants (clone #s 3, 4, or 27) for binding to human tonsil CD19+ cells. Expression of h16445 as detected by staining with the h16445-specific hybridoma supernatants (peak 2) is shown relative to that detected by staining with an
25 irrelevant antibody supernatant specific for the chemokine neurotactin (Nt) (peak 1).

DETAILED DESCRIPTION OF THE INVENTION

30 The present invention provides isolated nucleic acid molecules comprising nucleotide sequences encoding the IL-9/IL-2 receptor-like polypeptides whose amino acid sequences are given in SEQ ID NO:2 and SEQ ID NO:4, or a variant or fragment of the polypeptides. Nucleotide sequences encoding the IL-9/IL-2

receptor-like polypeptides of the invention are set forth in SEQ ID NO:1 and SEQ ID NO:3.

The disclosed invention relates to methods and compositions for the modulation, diagnosis, and treatment of immune, inflammatory, and respiratory disorders, and disorders associated with the lungs, colon, kidney, and lymphoid tissues, including tonsil and thymus. Immune disorders include, but are not limited to, chronic inflammatory diseases and disorders, such as Crohn's disease, rheumatoid arthritis, reactive arthritis, including Lyme disease, insulin-dependent diabetes, organ-specific autoimmunity, including multiple sclerosis, Hashimoto's thyroiditis and Grave's disease, contact dermatitis, psoriasis, graft rejection, graft versus host disease, sarcoidosis, atopic conditions, such as asthma and allergy, including allergic rhinitis, gastrointestinal allergies, including food allergies, eosinophilia, conjunctivitis, glomerular nephritis, certain pathogen susceptibilities such as helminthic (e.g., leishmaniasis), certain viral infections, including HIV, and bacterial infections, including tuberculosis and lepromatous leprosy.

Respiratory disorders include, but are not limited to, apnea, asthma, particularly bronchial asthma, berillium disease, bronchiectasis, bronchitis, bronchopneumonia, cystic fibrosis, diphtheria, dyspnea, emphysema, chronic obstructive pulmonary disease, allergic bronchopulmonary aspergillosis, pneumonia, acute pulmonary edema, pertussis, pharyngitis, atelectasis, Wegener's granulomatosis, Legionnaires disease, pleurisy, rheumatic fever, and sinusitis.

Disorders involving the lung include, but are not limited to, congenital anomalies; atelectasis; diseases of vascular origin, such as pulmonary congestion and edema, including hemodynamic pulmonary edema and edema caused by microvascular injury, adult respiratory distress syndrome (diffuse alveolar damage), pulmonary embolism, hemorrhage, and infarction, and pulmonary hypertension and vascular sclerosis; chronic obstructive pulmonary disease, such as emphysema, chronic bronchitis, bronchial asthma, and bronchiectasis; diffuse interstitial (infiltrative, restrictive) diseases, such as pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia (pulmonary infiltration with eosinophilia), *Bronchiolitis obliterans*-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, including Goodpasture syndrome, idiopathic pulmonary

hemosiderosis and other hemorrhagic syndromes, pulmonary involvement in collagen vascular disorders, and pulmonary alveolar proteinosis; complications of therapies, such as drug-induced lung disease, radiation-induced lung disease, and lung transplantation; tumors, such as bronchogenic carcinoma, including
5 paraneoplastic syndromes, bronchioloalveolar carcinoma, neuroendocrine tumors, such as bronchial carcinoid, miscellaneous tumors, and metastatic tumors; pathologies of the pleura, including inflammatory pleural effusions, noninflammatory pleural effusions, pneumothorax, and pleural tumors, including solitary fibrous tumors (pleural fibroma) and malignant mesothelioma.

10 Disorders involving the colon include, but are not limited to, congenital anomalies, such as atresia and stenosis, Meckel diverticulum, congenital aganglionic megacolon-Hirschsprung disease; enterocolitis, such as diarrhea and dysentery, infectious enterocolitis, including viral gastroenteritis, bacterial enterocolitis, necrotizing enterocolitis, antibiotic-associated colitis
15 (pseudomembranous colitis), and collagenous and lymphocytic colitis, miscellaneous intestinal inflammatory disorders, including parasites and protozoa, acquired immunodeficiency syndrome, transplantation, drug-induced intestinal injury, radiation enterocolitis, neutropenic colitis (typhlitis), and diversion colitis; idiopathic inflammatory bowel disease, such as Crohn disease and ulcerative
20 colitis; tumors of the colon, such as non-neoplastic polyps, adenomas, familial syndromes, colorectal carcinogenesis, colorectal carcinoma, and carcinoid tumors.

Disorders involving the kidney include, but are not limited to, congenital anomalies including, but not limited to, cystic diseases of the kidney, that include but are not limited to, cystic renal dysplasia, autosomal dominant (adult) polycystic
25 kidney disease, autosomal recessive (childhood) polycystic kidney disease, and cystic diseases of renal medulla, which include, but are not limited to, medullary sponge kidney, and nephronophthisis-uremic medullary cystic disease complex, acquired (dialysis-associated) cystic disease, such as simple cysts; glomerular diseases including pathologies of glomerular injury that include, but are not limited to, in situ
30 immune complex deposition, that includes, but is not limited to, anti-GBM nephritis, Heymann nephritis, and antibodies against planted antigens, circulating immune complex nephritis, antibodies to glomerular cells, cell-mediated immunity in glomerulonephritis, activation of alternative complement pathway, epithelial cell

injury, and pathologies involving mediators of glomerular injury including cellular and soluble mediators, acute glomerulonephritis, such as acute proliferative (poststreptococcal, postinfectious) glomerulonephritis, including but not limited to, poststreptococcal glomerulonephritis and nonstreptococcal acute glomerulonephritis, rapidly progressive (crescentic) glomerulonephritis, nephrotic syndrome, membranous glomerulonephritis (membranous nephropathy), minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis, membranoproliferative glomerulonephritis, IgA nephropathy (Berger disease), focal proliferative and necrotizing glomerulonephritis (focal glomerulonephritis), hereditary nephritis, including but not limited to, Alport syndrome and thin membrane disease (benign familial hematuria), chronic glomerulonephritis, glomerular lesions associated with systemic disease, including but not limited to, systemic lupus erythematosus, Henoch-Schönlein purpura, bacterial endocarditis, diabetic glomerulosclerosis, amyloidosis, fibrillary and immunotactoid glomerulonephritis, and other systemic disorders; diseases affecting tubules and interstitium, including acute tubular necrosis and tubulointerstitial nephritis, including but not limited to, pyelonephritis and urinary tract infection, acute pyelonephritis, chronic pyelonephritis and reflux nephropathy, and tubulointerstitial nephritis induced by drugs and toxins, including but not limited to, acute drug-induced interstitial nephritis, analgesic abuse nephropathy, nephropathy associated with nonsteroidal anti-inflammatory drugs, and other tubulointerstitial diseases including, but not limited to, urate nephropathy, hypercalcemia and nephrocalcinosis, and multiple myeloma; diseases of blood vessels including benign nephrosclerosis, malignant hypertension and accelerated nephrosclerosis, renal artery stenosis, and thrombotic microangiopathies including, but not limited to, classic (childhood) hemolytic-uremic syndrome, adult hemolytic-uremic syndrome/thrombotic thrombocytopenic purpura, idiopathic HUS/TTP, and other vascular disorders including, but not limited to, atherosclerotic ischemic renal disease, atheroembolic renal disease, sickle cell disease nephropathy, diffuse cortical necrosis, and renal infarcts; urinary tract obstruction (obstructive uropathy); urolithiasis (renal calculi, stones); and tumors of the kidney including, but not limited to, benign tumors, such as renal papillary adenoma, renal fibroma or hamartoma (renomedullary interstitial cell tumor), angiomyolipoma, and oncocytoma, and malignant tumors, including renal

cell carcinoma (hypernephroma, adenocarcinoma of kidney), which includes urothelial carcinomas of renal pelvis.

Disorders involving the thymus include developmental disorders, such as DiGeorge syndrome with thymic hypoplasia or aplasia; thymic cysts; thymic hypoplasia, which involves the appearance of lymphoid follicles within the thymus, creating thymic follicular hyperplasia; and thymomas, including germ cell tumors, lymphomas, Hodgkin disease, and carcinoids. Thymomas can include benign or encapsulated thymoma, and malignant thymoma Type I (invasive thymoma) or Type II, designated thymic carcinoma.

The invention is also directed to methods and compositions for the modulation, diagnosis, and treatment of disorders associated with lymphoid cells including B- and T-cells. These disorders include, but are not limited to, the leukemias, including B-lymphoid leukemias, T-lymphoid leukemias, undifferentiated leukemias; precursor B-cell neoplasms, such as lymphoblastic leukemia/lymphoma; peripheral B-cell neoplasms, including, but not limited to, chronic lymphocytic leukemia/small lymphocytic lymphoma, follicular lymphoma, diffuse large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, multiple myeloma, and related entities, lymphoplasmacytic lymphoma (Waldenström macroglobulinemia), mantle cell lymphoma, marginal zone lymphoma (MALToma), and hairy cell leukemia.

A novel human full-length cDNA, termed clone h16445, and its murine orthologue, termed clone m16445, are provided. Such sequences are referred to as "IL-9/IL-2 receptor-like" indicating that they share sequence similarity to the IL-9 and IL-2 receptor genes.

The sequences of the invention find use in modulating an immune response. By "modulating" is intended the upregulating or downregulating of a response. That is, the compositions of the invention, affect the targeted activity in either a positive or negative fashion. The activation of T cells is manifested by lymphokine production, cellular proliferation, signaling events, and other effector functions.

The function of T cells is defined by the type of cytokines released upon antigenic challenge. Such cytokines are central to disease evolution in animal

models of autoimmunity and infection. Proteins and/or antibodies of the invention are also useful in modulating immune, inflammatory and respiratory responses.

The IL-9/IL-2 receptor-like cDNA, clone h16445, and its murine orthologue, m16445, were identified in a human peripheral blood lymphocyte cDNA library and a mouse LTBM (long-term bone marrow cell) cDNA library, respectively. Clone h16445 encodes an approximately 2.3 Kb mRNA transcript having the corresponding cDNA set forth in SEQ ID NO:1. This transcript has a 1614 nucleotide open reading frame (nucleotides 349-1965 of SEQ ID NO:1), which encodes a 538 amino acid protein (SEQ ID NO:2) having a molecular weight of approximately 59.1 kDa. An analysis of the full-length h16445 polypeptide predicts that the N-terminal 19 amino acids represent a signal peptide. Transmembrane segments from amino acids (aa) 9-26 and 425-446 were predicted by MEMSAT. Transmembrane segments were also predicted from aa 219-236 and 406-427 of the presumed mature peptide sequence. Prosite program analysis was used to predict various sites within the h16445 protein. N-glycosylation sites were predicted at aa 73-76, 97-100, 104-107, 125-128, and 135-138. A cAMP- and cGMP-dependent protein kinase phosphorylation site was predicted at aa 191-194. Protein kinase C phosphorylation sites were predicted at aa 117-119, 137-139, 170-172, and 254-256. Casein kinase II phosphorylation sites were predicted at aa 50-53, 140-143, 194-197, 213-216, 225-228, 299-302, 312-315, 380-383, 393-396, 444-447, 474-477, 501-504, and 509-512. A tyrosine kinase phosphorylation site was predicted at aa 153-160. N-myristoylation sites were predicted at aa 293-298, 360-365, 429-434, 439-444, 462-467, 472-477, 479-484, and 496-501.

An RGD cell attachment sequence was predicted at aa 163-165. A growth factor and cytokine receptor signature 2 sequence was predicted at aa 212-218. The IL-9/IL-2 receptor-like protein possesses a fibronectin type III domain, from aa 120-215, and a U-PAR/Ly-6 domain, from aa 230-255, as predicted by HMMer, Version 2. The fibronectin type III domain is one of three types of internal repeats within the plasma protein fibronectin. The tenth fibronectin type III repeat contains an RGD cell recognition sequence in a flexible loop between two strands. Type III modules are present in both extracellular and intracellular proteins. See, for example, Petersen *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:137-141. The U-PAR/Ly-6 domain is a urokinase plasminogen activator surface receptor involved

in binding urokinase plasminogen activator. This domain is responsible for signal transduction and is found in the family of Ly-6 T-cell antigens. See, for example, Behrendt *et al.* (1991) *J. Biol. Chem.* 266:7842-7847, and Ploug *et al.* (1993) *J. Biol. Chem.* 268:17539-17546.

5 The h16445 protein displays similarity to the human IL-2 receptor beta chain (SEQ ID NO:5; approximately 36.9% identity over a 130 amino acid overlap), the murine IL-2 receptor beta chain (SEQ ID NO:6; 32.7% identity over a 110 amino acid overlap), the human IL-9 receptor (SEQ ID NO:7; approximately 29.7% identity over a 158 amino acid overlap), and the murine IL-9 receptor (SEQ
10 ID NO:8; approximately 28.3% identity over a 166 amino acid overlap) (see Figure 1).

A plasmid containing the h16445 cDNA insert was deposited with American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Virginia, on July 14, 1999, and assigned Accession Number PTA-350.
15 This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. § 112.

20 The murine clone, m16445, encodes an approximately 2.5 Kb mRNA transcript having the corresponding cDNA set forth in SEQ ID NO:3. This transcript has a 1587 nucleotide open reading frame (nucleotides 391-1976 of SEQ ID NO:3), which encodes a 529 amino acid protein (SEQ ID NO:4) having a molecular weight of approximately 58.3 kDa. An analysis of the full-length
25 m16445 polypeptide predicts that the N-terminal 19 amino acids represent a signal peptide. This polypeptide represents the protein sequence encoded by the murine orthologue of the h16445 gene. The mouse 16445 protein shares approximately 64.4% identity with the human 16445 protein disclosed in SEQ ID NO:2 (see Figure 1).

30 An analysis of the disclosed m16445 polypeptide sequence (SEQ ID NO:4) using the MEMSAT program predicts transmembrane segments from amino acids (aa) 7-23 and 415-434. Transmembrane segments were also predicted from aa 219-235 and 396-415 of the presumed mature peptide sequence. Prosite program

analysis was also used to predict various sites within the m16445 protein sequence. N-glycosylation sites were predicted at 73-76, 97-100, 104-107, 125-128, and 182-185. A glycosaminoglycan attachment site was predicted from aa 430-433. Protein kinase C phosphorylation sites were predicted at aa 117-119, 131-133, and 209-211. Casein kinase II phosphorylation sites were predicted at aa 19-22, 50-53, 140-143, 213-216, 299-302, 378-381, 391-394, 442-445, 472-475, and 498-501. A tyrosine kinase phosphorylation site was predicted at 153-160. N-myristoylation sites were predicted at 16-21, 355-360, 427-432, 433-438, 466-471, 477-482, and 493-498. A growth factor and cytokine receptor signature 2 sequence was predicted at aa 212-218. Analysis with HMMer, Version 2, predicted a fibronectin type III domain from aa 120-215 in the mouse IL-9/IL-2 receptor-like protein, similar to that described for the human 16445 protein. A FN3_2 domain from aa 120-209 was also predicted for this protein by HMMer analysis.

The IL-9/IL-2 receptor-like sequences of the invention are members of a family of molecules (the "Type 1 cytokine receptor family") having conserved functional features. The term "family" when referring to the proteins and nucleic acid molecules of the invention is intended to mean two or more proteins or nucleic acid molecules having sufficient amino acid or nucleotide sequence identity as defined herein. Such family members can be naturally occurring and can be from either the same or different species. For example, a family can contain a first protein of murine origin and a homologue of that protein of human origin, as well as a second, distinct protein of human origin and a murine homologue of that protein. Members of a family may also have common functional characteristics.

Preferred IL-9/IL-2 receptor-like polypeptides of the present invention have an amino acid sequence sufficiently identical to the amino acid sequence of SEQ ID NO:2 or 4. The term "sufficiently identical" is used herein to refer to a first amino acid or nucleotide sequence that contains a sufficient or minimum number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have a common structural domain and/or common functional activity. For example, amino acid or nucleotide sequences that contain a common structural domain having at least about 45%, 55%, or 65% identity, preferably 70% identity, more preferably 80%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97% or 98% identity are defined herein as sufficiently identical.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent identity = number of identical positions/total number of positions (e.g., overlapping positions) x 100). In one embodiment, the two sequences are the same length. The percent identity between two sequences can be determined using techniques similar to those described below, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to IL-9/IL-2 receptor-like nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to IL-9/IL-2 receptor-like protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence

alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Accordingly, another embodiment of the invention features isolated IL-9/IL-2 receptor-like proteins and polypeptides having an IL-9/IL-2 receptor-like protein activity. As used interchangeably herein, a "IL-9/IL-2 receptor-like protein activity", "biological activity of an IL-9/IL-2 receptor-like protein", or "functional activity of an IL-9/IL-2 receptor-like protein" refers to an activity exerted by an IL-9/IL-2 receptor-like protein, polypeptide, or nucleic acid molecule on an IL-9/IL-2 receptor-like responsive cell as determined *in vivo*, or *in vitro*, according to standard assay techniques. An IL-9/IL-2 receptor-like activity can be a direct activity, such as an association with or an enzymatic activity on a second protein, or an indirect activity, such as a cellular signaling activity mediated by interaction of the IL-9/IL-2 receptor-like protein with a second protein. In a preferred embodiment, an IL-9/IL-2 receptor-like activity includes at least one or more of the following activities: (1) modulating (stimulating and/or enhancing or inhibiting) cellular proliferation, differentiation, and/or function, particularly immune cells, for example lymphocytes, such as B cells, plasma cells, T cells, and null cells, macrophages, histiocytes, and granulocytes, such as neutrophils, eosinophils, basophils, and tissue mast cells; (2) modulating an IL-9/IL-2 receptor-like immune response; (3) modulating an inflammatory response; (4) modulating a respiratory response; and (5) binding an IL-9 or IL-2 receptor ligand.

An "isolated" or "purified" IL-9/IL-2 receptor-like nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For purposes of the invention, "isolated" when used to refer to nucleic acid molecules excludes isolated chromosomes. For example, in various embodiments, the isolated IL-9/IL-2 receptor-like nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2

kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. An IL-9/IL-2 receptor-like protein that is substantially free of cellular material includes preparations of IL-9/IL-2 receptor-like protein having less than about 5 30%, 20%, 10%, or 5% (by dry weight) of non-IL-9/IL-2 receptor-like protein (also referred to herein as a "contaminating protein"). When the IL-9/IL-2 receptor-like protein or biologically active portion thereof is recombinantly produced, preferably, culture medium represents less than about 30%, 20%, 10%, or 5% of the volume of the protein preparation. When IL-9/IL-2 receptor-like 10 protein is produced by chemical synthesis, preferably the protein preparations have less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-IL-9/IL-2 receptor-like chemicals.

Various aspects of the invention are described in further detail in the following subsections.

15

1. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules comprising nucleotide sequences encoding IL-9/IL-2 receptor-like proteins and polypeptides or biologically active portions thereof, as well as nucleic acid 20 molecules sufficient for use as hybridization probes to identify IL-9/IL-2 receptor-like-encoding nucleic acids (e.g., IL-9/IL-2 receptor-like mRNA) and fragments for use as PCR primers for the amplification or mutation of IL-9/IL-2 receptor-like nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA 25 molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

Nucleotide sequences encoding the IL-9/IL-2 receptor-like proteins of the present invention include sequences set forth in SEQ ID NO:1 and SEQ ID NO:3, 30 the nucleotide sequence of the cDNA insert of the plasmid deposited with the ATCC as Accession Number PTA-350 (the "cDNA of ATCC PTA-350"), and complements thereof. By "complement" is intended a nucleotide sequence that is sufficiently complementary to a given nucleotide sequence such that it can

hybridize to the given nucleotide sequence to thereby form a stable duplex. The corresponding amino acid sequences for the IL-9/IL-2 receptor-like proteins encoded by these nucleotide sequences are set forth in SEQ ID NO:2 and SEQ ID NO:4.

5 Nucleic acid molecules that are fragments of these IL-9/IL-2 receptor-like nucleotide sequences are also encompassed by the present invention. By "fragment" is intended a portion of the nucleotide sequence encoding an IL-9/IL-2 receptor-like protein. A fragment of an IL-9/IL-2 receptor-like nucleotide sequence may encode a biologically active portion of an IL-9/IL-2 receptor-like protein, or it may be a fragment that can be used as a hybridization probe or PCR primer using methods disclosed below. A biologically active portion of an IL-9/IL-2 receptor-like protein can be prepared by isolating a portion of one of the IL-9/IL-2 receptor-like nucleotide sequences of the invention, expressing the encoded portion of the IL-9/IL-2 receptor-like protein (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the IL-9/IL-2 receptor-like protein. Nucleic acid molecules that are fragments of an IL-9/IL-2 receptor-like nucleotide sequence comprise at least 15, 20, 50, 75, 100, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400 nucleotides, or up to the number of nucleotides present in a full-length IL-9/IL-2 receptor-like nucleotide sequence disclosed herein (for example, 2343 or 2456 nucleotides for SEQ ID NO:1 or SEQ ID NO:3, respectively) depending upon the intended use.

It is understood that isolated fragments include any contiguous sequence not disclosed prior to the invention as well as sequences that are substantially the same and which are not disclosed. Accordingly, if an isolated fragment is disclosed prior to the present invention, that fragment is not intended to be encompassed by the invention. When a sequence is not disclosed prior to the present invention, an isolated nucleic acid fragment is at least about 12, 15, 20, 25, or 30 contiguous nucleotides. Other regions of the nucleotide sequence may comprise fragments of various sizes, depending upon potential homology with previously disclosed sequences.

For example, when considering the open reading frame of SEQ ID NO:1 (nt 349-1965), the nucleotide sequence from about 349 to about 398 encompasses

isolated fragments greater than about 25, 27, or 30 nucleotides; the nucleotide sequence from about 398 to about 508 encompasses isolated fragments greater than about 106, 107, or 108 nucleotides; the nucleotide sequence from about 508 to about 858 encompasses isolated fragments greater than about 201, 205, or 210
5 nucleotides; the nucleotide sequence from about 858 to about 1158 encompasses isolated fragments greater than about 179, 185, or 190 nucleotides; the nucleotide sequence from about 1158 to about 1965 encompasses isolated fragments greater than about 752, 755, or 780 nucleotides.

A fragment of an IL-9/IL-2 receptor-like nucleotide sequence that encodes
10 a biologically active portion of an IL-9/IL-2 receptor-like protein of the invention will encode at least 15, 25, 30, 50, 75, 100, 125, 150, 175, 200, 250, or 300 contiguous amino acids, or up to the total number of amino acids present in a full-length IL-9/IL-2 receptor-like protein of the invention (for example, 538 amino acids for SEQ ID NO:2, or 529 amino acids for SEQ ID NO:4). Fragments of an
15 IL-9/IL-2 receptor-like nucleotide sequence that are useful as hybridization probes for PCR primers generally need not encode a biologically active portion of an IL-9/IL-2 receptor-like protein.

Nucleic acid molecules that are variants of the IL-9/IL-2 receptor-like nucleotide sequences disclosed herein are also encompassed by the present
20 invention. "Variants" of the IL-9/IL-2 receptor-like nucleotide sequences include those sequences that encode the IL-9/IL-2 receptor-like proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code. These naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR) and
25 hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the IL-9/IL-2 receptor-like proteins disclosed in the present invention as discussed below. Generally, nucleotide sequence variants of the invention will have at least 45%,
30 55%, 65%, 75%, 85%, 95%, or 98% identity to a particular nucleotide sequence disclosed herein. A variant IL-9/IL-2 receptor-like nucleotide sequence will encode an IL-9/IL-2 receptor-like protein that has an amino acid sequence having at least 45%, 55%, 65%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97% or 98% identity to the amino acid sequence of an IL-9/IL-2 receptor-like protein disclosed herein.

In addition to the IL-9/IL-2 receptor-like nucleotide sequences shown in SEQ ID NOs:1 and 3, and the nucleotide sequence of the cDNA of ATCC PTA-350, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of IL-9/IL-2 receptor-like proteins may exist within a population (e.g., the human population). Such genetic polymorphism in an IL-9/IL-2 receptor-like gene may exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes that occur alternatively at a given genetic locus. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an IL-9/IL-2 receptor-like protein, preferably a mammalian IL-9/IL-2 receptor-like protein. As used herein, the phrase "allelic variant" refers to a nucleotide sequence that occurs at an IL-9/IL-2 receptor-like locus or to a polypeptide encoded by the nucleotide sequence. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the IL-9/IL-2 receptor-like gene. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations in an IL-9/IL-2 receptor-like sequence that are the result of natural allelic variation and that do not alter the functional activity of IL-9/IL-2 receptor-like proteins are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding IL-9/IL-2 receptor-like proteins from other species (IL-9/IL-2 receptor-like homologues), which have a nucleotide sequence differing from that of the IL-9/IL-2 receptor-like sequences disclosed herein, are intended to be within the scope of the invention. For example, nucleic acid molecules corresponding to natural allelic variants and homologues of the human IL-9/IL-2 receptor-like cDNA of the invention can be isolated based on their identity to the human IL-9/IL-2 receptor-like nucleic acid disclosed herein using the human cDNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions as disclosed below.

In addition to naturally-occurring allelic variants of the IL-9/IL-2 receptor-like sequences that may exist in the population, the skilled artisan will further

appreciate that changes can be introduced by mutation into the nucleotide sequences of the invention thereby leading to changes in the amino acid sequence of the encoded IL-9/IL-2 receptor-like proteins, without altering the biological activity of the IL-9/IL-2 receptor-like proteins. Thus, an isolated nucleic acid molecule encoding an IL-9/IL-2 receptor-like protein having a sequence that differs from that of SEQ ID NO:2 or 4 can be created by introducing one or more nucleotide substitutions, additions, or deletions into the corresponding nucleotide sequence disclosed herein, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Such variant nucleotide sequences are also encompassed by the present invention.

For example, preferably, conservative amino acid substitutions may be made at one or more predicted, preferably nonessential amino acid residues. A "nonessential" amino acid residue is a residue that can be altered from the wild-type sequence of an IL-9/IL-2 receptor-like protein (e.g., the sequence of SEQ ID NO:2 or 4) without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, such as the growth factor and cytokine receptor signature 2 sequence of SEQ ID NO:2 and 4 and the U-PAR/Ly-6 domain sequence of SEQ ID NO:2, where such residues are essential for protein activity.

Alternatively, variant IL-9/IL-2 receptor-like nucleotide sequences can be made by introducing mutations randomly along all or part of an IL-9/IL-2 receptor-

like coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for IL-9/IL-2 receptor-like biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly, and the activity of the protein can be determined using standard
5 assay techniques.

Thus the nucleotide sequences of the invention include the sequences disclosed herein as well as fragments and variants thereof. The IL-9/IL-2 receptor-like nucleotide sequences of the invention, and fragments and variants thereof, can be used as probes and/or primers to identify and/or clone IL-9/IL-2 receptor-like
10 homologues in other cell types, e.g., from other tissues, as well as IL-9/IL-2 receptor-like homologues from other mammals. Such probes can be used to detect transcripts or genomic sequences encoding the same or identical proteins. These probes can be used as part of a diagnostic test kit for identifying cells or tissues that misexpress an IL-9/IL-2 receptor-like protein, such as by measuring levels of
15 an IL-9/IL-2 receptor-like-encoding nucleic acid in a sample of cells from a subject, e.g., detecting IL-9/IL-2 receptor-like mRNA levels or determining whether a genomic IL-9/IL-2 receptor-like gene has been mutated or deleted.

In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences having substantial identity to the sequences of the
20 invention. See, for example, Sambrook *et al.* (1989) *Molecular Cloning: Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, NY) and Innis, *et al.* (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, NY). IL-9/IL-2 receptor-like nucleotide sequences isolated based on their sequence identity to the IL-9/IL-2 receptor-like nucleotide
25 sequences set forth herein or to fragments and variants thereof are encompassed by the present invention.

In a hybridization method, all or part of a known IL-9/IL-2 receptor-like nucleotide sequence can be used to screen cDNA or genomic libraries. Methods for construction of such cDNA and genomic libraries are generally known in the
30 art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, NY). The so-called hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable

group such as ^{32}P , or any other detectable marker, such as other radioisotopes, a fluorescent compound, an enzyme, or an enzyme co-factor. Probes for hybridization can be made by labeling synthetic oligonucleotides based on the known IL-9/IL-2 receptor-like nucleotide sequence disclosed herein. Degenerate primers designed on the basis of conserved nucleotides or amino acid residues in a known IL-9/IL-2 receptor-like nucleotide sequence or encoded amino acid sequence can additionally be used. The probe typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 consecutive nucleotides of an IL-9/IL-2 receptor-like nucleotide sequence of the invention or a fragment or variant thereof. Preparation of probes for hybridization is generally known in the art and is disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York), herein incorporated by reference.

For example, in one embodiment, a previously unidentified IL-9/IL-2 receptor-like nucleic acid molecule hybridizes under stringent conditions to a probe that is a nucleic acid molecule comprising one of the IL-9/IL-2 receptor-like nucleotide sequences of the invention or a fragment thereof. In another embodiment, the previously unknown IL-9/IL-2 receptor-like nucleic acid molecule is at least 300, 325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 2,000, 3,000, 4,000 or 5,000 nucleotides in length and hybridizes under stringent conditions to a probe that is a nucleic acid molecule comprising one of the IL-9/IL-2 receptor-like nucleotide sequences disclosed herein or a fragment thereof.

Accordingly, in another embodiment, an isolated previously unknown IL-9/IL-2 receptor-like nucleic acid molecule of the invention is at least 300, 325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1,100, 1,200, 1,300, or 1,400 nucleotides in length and hybridizes under stringent conditions to a probe that is a nucleic acid molecule comprising one of the nucleotide sequences of the invention, preferably the coding sequence set forth in SEQ ID NO:1 or 3, the cDNA of ATCC PTA-350, or a complement, fragment, or variant thereof.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences having at least 60%, 65%, 70%, preferably 75% identity to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology* (John Wiley & Sons, New York (1989)), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. In another preferred embodiment, stringent conditions comprise hybridization in 6 X SSC at 42°C, followed by washing with 1 X SSC at 55°C. Preferably, an isolated nucleic acid molecule that hybridizes under stringent conditions to an IL-9/IL-2 receptor-like sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

Thus, in addition to the IL-9/IL-2 receptor-like nucleotide sequences disclosed herein and fragments and variants thereof, the isolated nucleic acid molecules of the invention also encompass homologous DNA sequences identified and isolated from other cells and/or organisms by hybridization with entire or partial sequences obtained from the IL-9/IL-2 receptor-like nucleotide sequences disclosed herein or variants and fragments thereof.

The present invention also encompasses antisense nucleic acid molecules, i.e., molecules that are complementary to a sense nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule, or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire IL-9/IL-2 receptor-like coding strand, or to only a portion thereof, e.g., all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can be antisense to a noncoding region of the coding strand of a nucleotide sequence encoding an IL-9/IL-2 receptor-like protein. The noncoding regions are the 5' and 3' sequences that flank the coding region and are not translated into amino acids.

Given the coding-strand sequence encoding an IL-9/IL-2 receptor-like protein disclosed herein (e.g., SEQ ID NO:1 or 3), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding
5 region of IL-9/IL-2 receptor-like mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of IL-9/IL-2 receptor-like mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of IL-9/IL-2 receptor-like mRNA. An antisense oligonucleotide can be, for example, about 5,
10 10, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation procedures known in the art.

For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously
15 modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, including, but not limited to, for example e.g., phosphorothioate derivatives and acridine substituted nucleotides. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector
20 into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind
25 to cellular mRNA and/or genomic DNA encoding an IL-9/IL-2 receptor-like protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected
30 cells and then administered systemically. For example, antisense molecules can be linked to peptides or antibodies to form a complex that specifically binds to receptors or antigens expressed on a selected cell surface. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein.

To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes, which are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave IL-9/IL-2 receptor-like mRNA transcripts to thereby inhibit translation of IL-9/IL-2 receptor-like mRNA. A ribozyme having specificity for an IL-9/IL-2 receptor-like-encoding nucleic acid can be designed based upon the nucleotide sequence of an IL-9/IL-2 receptor-like cDNA disclosed herein (e.g., SEQ ID NO:1 or 3). *See*, e.g., Cech *et al.*, U.S. Patent No. 4,987,071; and Cech *et al.*, U.S. Patent No. 5,116,742. Alternatively, IL-9/IL-2 receptor-like mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See*, e.g., Bartel and Szostak (1993) *Science* 261:1411-1418.

The invention also encompasses nucleic acid molecules that form triple helical structures. For example, IL-9/IL-2 receptor-like gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the IL-9/IL-2 receptor-like protein (e.g., the IL-9/IL-2 receptor-like promoter and/or enhancers) to form triple helical structures that prevent transcription of the IL-9/IL-2 receptor-like gene in target cells. *See generally* Helene (1991) *Anticancer Drug Des.* 6(6):569; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27; and Maher (1992) *Bioassays* 14(12):807.

In preferred embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety, or phosphate backbone to improve,

e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (*see Hyrup et al. (1996) Bioorganic & Medicinal Chemistry* 4:5). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid-phase peptide synthesis protocols as described in Hyrup *et al. (1996), supra*; Perry-O'Keefe *et al. (1996) Proc. Natl. Acad. Sci. USA* 93:14670.

PNAs of an IL-9/IL-2 receptor-like molecule can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA-directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup (1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup (1996), *supra*; Perry-O'Keefe *et al. (1996), supra*).

In another embodiment, PNAs of an IL-9/IL-2 receptor-like molecule can be modified, e.g., to enhance their stability, specificity, or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*; Finn *et al. (1996) Nucleic Acids Res.* 24(17):3357-63; Mag *et al. (1989) Nucleic Acids Res.* 17:5973; and Peterson *et al. (1975) Bioorganic Med. Chem. Lett.* 5:1119.

II. Isolated IL-9/IL-2 Receptor-like Proteins and Anti-IL-9/IL-2 Receptor-like Antibodies

IL-9/IL-2 receptor-like proteins are also encompassed within the present invention. By "IL-9/IL-2 receptor-like protein" is intended a protein having the

amino acid sequence set forth in SEQ ID NO: 2 or SEQ ID NO:4, as well as fragments, biologically active portions, and variants thereof.

"Fragments" or "biologically active portions" include polypeptide fragments suitable for use as immunogens to raise anti-IL-9/IL-2 receptor-like antibodies. Fragments include peptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of an IL-9/IL-2 receptor-like protein of the invention and exhibiting at least one activity of an IL-9/IL-2 receptor-like protein, but which include fewer amino acids than the full-length SEQ ID NO:2 or SEQ ID NO:4 IL-9/IL-2 receptor-like proteins disclosed herein. Typically, biologically active portions comprise a domain or motif with at least one activity of the IL-9/IL-2 receptor-like protein. A biologically active portion of an IL-9/IL-2 receptor-like protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Such biologically active portions can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native IL-9/IL-2 receptor-like protein. As used here, a fragment comprises at least 5 contiguous amino acids, such as from amino acid (aa) 1 to 210 and aa 220 to 538 of SEQ ID NO:2. The invention encompasses other fragments, however, such as any fragment in the protein greater than 6, 7, 8, or 9 amino acids.

By "variants" is intended proteins or polypeptides having an amino acid sequence that is at least about 45%, 55%, 65%; preferably about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the amino acid sequence of SEQ ID NO:2 or 4. Variants also include polypeptides encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or polypeptides encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule of SEQ ID NO:1 or 3, or a complement thereof, under stringent conditions. Such variants generally retain the functional activity of the IL-9/IL-2 receptor-like proteins of the invention. Variants include polypeptides that differ in amino acid sequence due to natural allelic variation or mutagenesis.

The invention also provides IL-9/IL-2 receptor-like chimeric or fusion proteins. As used herein, an IL-9/IL-2 receptor-like "chimeric protein" or "fusion protein" comprises an IL-9/IL-2 receptor-like polypeptide operably linked to a non-IL-9/IL-2 receptor-like polypeptide. A "IL-9/IL-2 receptor-like polypeptide"

refers to a polypeptide having an amino acid sequence corresponding to an IL-9/IL-2 receptor-like protein, whereas a "non-IL-9/IL-2 receptor-like polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially identical to the IL-9/IL-2 receptor-like protein, e.g., a
5 protein that is different from the IL-9/IL-2 receptor-like protein and which is derived from the same or a different organism. Within an IL-9/IL-2 receptor-like fusion protein, the IL-9/IL-2 receptor-like polypeptide can correspond to all or a portion of an IL-9/IL-2 receptor-like protein, preferably at least one biologically active portion of an IL-9/IL-2 receptor-like protein. Within the fusion protein, the
10 term "operably linked" is intended to indicate that the IL-9/IL-2 receptor-like polypeptide and the non-IL-9/IL-2 receptor-like polypeptide are fused in-frame to each other. The non-IL-9/IL-2 receptor-like polypeptide can be fused to the N-terminus or C-terminus of the IL-9/IL-2 receptor-like polypeptide.

One useful fusion protein is a GST-IL-9/IL-2 receptor-like fusion protein in
15 which the IL-9/IL-2 receptor-like sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant IL-9/IL-2 receptor-like proteins.

In yet another embodiment, the fusion protein is an IL-9/IL-2 receptor-like-immunoglobulin fusion protein in which all or part of an IL-9/IL-2 receptor-like
20 protein is fused to sequences derived from a member of the immunoglobulin protein family. The IL-9/IL-2 receptor-like-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an IL-9/IL-2 receptor-like ligand and an IL-9/IL-2 receptor-like protein on the surface of a cell, thereby suppressing IL-
25 9/IL-2 receptor-like-mediated signal transduction *in vivo*. The IL-9/IL-2 receptor-like-immunoglobulin fusion proteins can be used to affect the bioavailability of an IL-9/IL-2 receptor-like cognate ligand. Inhibition of the IL-9/IL-2 receptor-like ligand/IL-9/IL-2 receptor-like interaction may be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (e.g.,
30 promoting or inhibiting) cell survival. Moreover, the IL-9/IL-2 receptor-like-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-IL-9/IL-2 receptor-like antibodies in a subject, to purify IL-9/IL-2 receptor-like ligands, and in screening assays to identify molecules that inhibit the

interaction of an IL-9/IL-2 receptor-like protein with an IL-9/IL-2 receptor-like ligand.

Preferably, an IL-9/IL-2 receptor-like chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences may be ligated
5 together in-frame, or the fusion gene can be synthesized, such as with automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments, which can subsequently be annealed and
10 reamplified to generate a chimeric gene sequence (*see, e.g., Ausubel et al., eds. (1995) Current Protocols in Molecular Biology*) (Greene Publishing and Wiley-Interscience, NY). Moreover, an IL-9/IL-2 receptor-like-encoding nucleic acid can be cloned into a commercially available expression vector such that it is linked in-frame to an existing fusion moiety. Variants of the IL-9/IL-2 receptor-like
15 proteins can function as either IL-9/IL-2 receptor-like agonists (mimetics) or as IL-9/IL-2 receptor-like antagonists. Variants of the IL-9/IL-2 receptor-like protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the IL-9/IL-2 receptor-like protein. An agonist of the IL-9/IL-2 receptor-like protein can retain substantially the same, or a subset, of the biological activities of the
20 naturally occurring form of the IL-9/IL-2 receptor-like protein. An antagonist of the IL-9/IL-2 receptor-like protein can inhibit one or more of the activities of the naturally occurring form of the IL-9/IL-2 receptor-like protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade that includes the IL-9/IL-2 receptor-like protein. Thus, specific biological
25 effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the IL-9/IL-2 receptor-like proteins.

Variants of an IL-9/IL-2 receptor-like protein that function as either IL-
30 9/IL-2 receptor-like agonists or as IL-9/IL-2 receptor-like antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of an IL-9/IL-2 receptor-like protein for IL-9/IL-2 receptor-like protein agonist or antagonist activity. In one embodiment, a variegated library of IL-9/IL-2 receptor-

like variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of IL-9/IL-2 receptor-like variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential IL-9/IL-2 receptor-like sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of IL-9/IL-2 receptor-like sequences therein. There are a variety of methods that can be used to produce libraries of potential IL-9/IL-2 receptor-like variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential IL-9/IL-2 receptor-like sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of an IL-9/IL-2 receptor-like protein coding sequence can be used to generate a variegated population of IL-9/IL-2 receptor-like fragments for screening and subsequent selection of variants of an IL-9/IL-2 receptor-like protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double-stranded PCR fragment of an IL-9/IL-2 receptor-like coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double-stranded DNA, renaturing the DNA to form double-stranded DNA which can include sense/antisense pairs from different nicked products, removing single-stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, one can derive an expression library that encodes N-terminal and internal fragments of various sizes of the IL-9/IL-2 receptor-like protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation and for screening cDNA libraries for gene products having a selected property. Such techniques are

adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of IL-9/IL-2 receptor-like proteins. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, 5 transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the 10 screening assays to identify IL-9/IL-2 receptor-like variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

An isolated IL-9/IL-2 receptor-like polypeptide of the invention can be used as an immunogen to generate antibodies that bind IL-9/IL-2 receptor-like 15 proteins using standard techniques for polyclonal and monoclonal antibody preparation. The full-length IL-9/IL-2 receptor-like protein can be used or, alternatively, the invention provides antigenic peptide fragments of IL-9/IL-2 receptor-like proteins for use as immunogens. The antigenic peptide of an IL-9/IL-2 receptor-like protein comprises at least 8, preferably 10, 15, 20, or 30 amino acid 20 residues of the amino acid sequence shown in SEQ ID NO:2 or 4 and encompasses an epitope of an IL-9/IL-2 receptor-like protein such that an antibody raised against the peptide forms a specific immune complex with the IL-9/IL-2 receptor-like protein. Preferred epitopes encompassed by the antigenic peptide are regions of a IL-9/IL-2 receptor-like protein that are located on the surface of the protein, 25 e.g., hydrophilic regions.

Accordingly, another aspect of the invention pertains to anti-IL-9/IL-2 receptor-like polyclonal and monoclonal antibodies that bind an IL-9/IL-2 receptor-like protein. Polyclonal anti-IL-9/IL-2 receptor-like antibodies can be prepared by immunizing a suitable subject (e.g., rabbit, goat, mouse, or other 30 mammal) with an IL-9/IL-2 receptor-like immunogen. The anti-IL-9/IL-2 receptor-like antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized IL-9/IL-2 receptor-like protein. At an appropriate

time after immunization, e.g., when the anti-IL-9/IL-2 receptor-like antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole *et al.* (1985) in *Monoclonal Antibodies and Cancer Therapy*, ed. Reisfeld and Sell (Alan R. Liss, Inc., New York, NY), pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally Coligan *et al.*, eds. (1994) *Current Protocols in Immunology* (John Wiley & Sons, Inc., New York, NY); Galfre *et al.* (1977) *Nature* 266:55052; Kenneth (1980) in *Monoclonal Antibodies: A New Dimension In Biological Analyses* (Plenum Publishing Corp., NY; and Lerner (1981) *Yale J. Biol. Med.*, 54:387-402).

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal anti-IL-9/IL-2 receptor-like antibody can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with an IL-9/IL-2 receptor-like protein to thereby isolate immunoglobulin library members that bind the IL-9/IL-2 receptor-like protein. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™ Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication Nos. WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; 93/01288; WO 92/01047; 92/09690; and 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

Additionally, recombinant anti-IL-9/IL-2 receptor-like antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and nonhuman portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in

the art, for example using methods described in PCT Publication Nos. WO 86101533 and WO 87/02671; European Patent Application Nos. 184,187, 171,496, 125,023, and 173,494; U.S. Patent Nos. 4,816,567 and 5,225,539; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521-3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Canc. Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced using transgenic mice that are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. See, for example, Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93; and U.S. Patent Nos. 5,625,126; 5,633,425; 5,569,825; 5,661,016; and 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies that recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. This technology is described by Jespers *et al.* (1994) *Bio/Technology* 12:899-903).

An anti-IL-9/IL-2 receptor-like antibody (e.g., monoclonal antibody) can be used to isolate IL-9/IL-2 receptor-like proteins by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-IL-9/IL-2 receptor-like antibody can facilitate the purification of natural IL-9/IL-2 receptor-like protein from cells and of recombinantly produced IL-9/IL-2 receptor-like protein expressed in host cells. Moreover, an anti-IL-9/IL-2 receptor-like antibody can be used to detect IL-9/IL-2 receptor-like protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the IL-

9/IL-2 receptor-like protein. Anti-IL-9/IL-2 receptor-like antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable
5 substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and
10 avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material
15 include ^{125}I , ^{131}I , ^{35}S , or ^3H .

Further, an antibody (or fragment thereof) may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine,
20 mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-
25 mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP)
30 cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine). The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to

classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, alpha-interferon, beta-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld *et al.* (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom *et al.*, "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson *et al.* (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera *et al.* (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin *et al.* (eds.), pp. 303-16 (Academic Press 1985), and Thorpe *et al.*, "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982). Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an IL-9/IL-2 receptor-like protein (or a portion thereof). "Vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked, such as a "plasmid", a circular double-stranded DNA loop into which additional DNA segments can be ligated, or a viral vector, where additional DNA segments can be ligated into the viral genome. The vectors are useful for autonomous replication in a host cell or may

be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome (e.g., nonepisomal mammalian vectors). Expression vectors are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors).
5 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), that serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, operably linked to the nucleic acid sequence to be expressed. "Operably linked" is intended to mean that the nucleotide sequence of interest is
15 linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers, and other expression control elements (e.g., polyadenylation signals). See, for example, Goeddel (1990) in *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, San Diego, CA). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that
25 the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., IL-9/IL-2 receptor-like proteins, mutant forms of IL-9/IL-2 receptor-like proteins, fusion proteins, etc.).
30

The recombinant expression vectors of the invention can be designed for expression of IL-9/IL-2 receptor-like protein in prokaryotic or eukaryotic host cells. Expression of proteins in prokaryotes is most often carried out in *E. coli*

with vectors containing constitutive or inducible promoters directing the expression of either fusion or nonfusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Typical fusion expression vectors include pGEX (Pharmacia
5 Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA), and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible nonfusion *E. coli* expression vectors include pTrc (Amann *et al.* (1988) *Gene*
10 69:301-315) and pET 11d (Studier *et al.* (1990) in *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, San Diego, CA), pp. 60-89). Strategies to maximize recombinant protein expression in *E. coli* can be found in Gottesman (1990) in *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, CA), pp. 119-128 and Wada *et al.* (1992) *Nucleic Acids Res.*
15 20:2111-2118. Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter.

Suitable eukaryotic host cells include insect cells (examples of Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the
20 pVL series (Lucklow and Summers (1989) *Virology* 170:31-39)); yeast cells (examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.* (1987) *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.* (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corporation, San
25 Diego, CA)); or mammalian cells (mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187:195)). Suitable mammalian cells include Chinese hamster ovary cells (CHO) or COS cells. In mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used
30 promoters are derived from polyoma, Adenovirus 2, cytomegalovirus, and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells, see chapters 16 and 17 of Sambrook *et al.* (1989) *Molecular cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press,

Plainview, NY). See, Goeddel (1990) in *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, San Diego, CA). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

5 The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences,

10 such progeny may not, in fact, be identical to the parent cell but are still included within the scope of the term as used herein.

 In one embodiment, the expression vector is a recombinant mammalian expression vector that comprises tissue-specific regulatory elements that direct expression of the nucleic acid preferentially in a particular cell type. Suitable
15 tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore
20 (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Patent Publication No. 264,166).
25 Developmentally-regulated promoters are also encompassed, for example the murine homeobox (Hox) promoter (Kessel and Gruss (1990) *Science* 249:374-379), the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546), and the like.

 The invention further provides a recombinant expression vector comprising
30 a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to IL-9/IL-2 receptor-like mRNA. Regulatory

sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen to direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen to direct constitutive, tissue-specific, or cell-type-specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.* (1986) *Reviews - Trends in Genetics*, Vol. 1(1).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, NY) and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin, and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an IL-9/IL-2 receptor-like protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) IL-9/IL-2 receptor-like protein.

Accordingly, the invention further provides methods for producing IL-9/IL-2 receptor-like protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention, into which a recombinant expression vector encoding an IL-9/IL-2 receptor-like protein has been introduced, in a suitable medium such that IL-9/IL-2 receptor-like protein is produced. In another embodiment, the method further comprises isolating IL-9/IL-2 receptor-like protein from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which IL-9/IL-2 receptor-like-coding sequences have been introduced. Such host cells can then be used to create nonhuman transgenic animals in which exogenous IL-9/IL-2 receptor-like sequences have been introduced into their genome or homologous recombinant animals in which endogenous IL-9/IL-2 receptor-like sequences have been altered. Such animals are useful for studying the function and/or activity of IL-9/IL-2 receptor-like genes and proteins and for identifying and/or evaluating modulators of IL-9/IL-2 receptor-like activity. As used herein, a "transgenic animal" is a nonhuman animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include nonhuman primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a nonhuman animal, preferably a mammal, more preferably a mouse, in which an endogenous IL-9/IL-2 receptor-like gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal. A transgenic animal of the invention can be created by introducing IL-9/IL-2 receptor-like-encoding nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The IL-9/IL-2 receptor-like cDNA sequence

can be introduced as a transgene into the genome of a nonhuman animal.

Alternatively, a homologue of the mouse IL-9/IL-2 receptor-like gene can be isolated based on hybridization and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the IL-9/IL-2 receptor-like transgene to direct expression of IL-9/IL-2 receptor-like protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866, 4,870,009, and 4,873,191 and in Hogan (1986) *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the IL-9/IL-2 receptor-like transgene in its genome and/or expression of IL-9/IL-2 receptor-like mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding IL-9/IL-2 receptor-like gene can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, one prepares a vector containing at least a portion of an IL-9/IL-2 receptor-like gene or a homolog of the gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the IL-9/IL-2 receptor-like gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous IL-9/IL-2 receptor-like gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous IL-9/IL-2 receptor-like gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous IL-9/IL-2 receptor-like protein). In the homologous recombination vector, the altered portion of the IL-9/IL-2 receptor-like gene is flanked at its 5' and 3' ends by additional nucleic acid of the IL-9/IL-2 receptor-like gene to allow for homologous

recombination to occur between the exogenous IL-9/IL-2 receptor-like gene carried by the vector and an endogenous IL-9/IL-2 receptor-like gene in an embryonic stem cell. The additional flanking IL-9/IL-2 receptor-like nucleic acid is of sufficient length for successful homologous recombination with the
5 endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (*see, e.g., Thomas and Capecchi (1987) Cell* 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g., by electroporation*), and cells in which the introduced IL-9/IL-2 receptor-like gene has homologously recombined
10 with the endogenous IL-9/IL-2 receptor-like gene are selected (*see, e.g., Li et al. (1992) Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g., a mouse*) to form aggregation chimeras (*see, e.g., Bradley (1987) in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, ed. Robertson (IRL, Oxford pp. 113-152)*). A chimeric embryo can then be implanted
15 into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous
20 recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic nonhuman animals containing selected systems that allow for regulated expression of the transgene can be produced. One
25 example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, *see, e.g., Lakso et al. (1992) Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al. (1991) Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to
30 regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g., by mating*

two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the nonhuman transgenic animals described herein can also be produced according to the methods described in Wilmot *et al.* (1997) *Nature*
5 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669.

IV. Pharmaceutical Compositions

The IL-9/IL-2 receptor-like nucleic acid molecules, IL-9/IL-2 receptor-like proteins, and anti-IL-9/IL-2 receptor-like antibodies (also referred to herein as
10 "active compounds") of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is
15 intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as
20 any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The compositions of the invention are useful to treat any of the disorders discussed herein. The compositions are provided in therapeutically effective amounts. By "therapeutically effective amounts" is intended an amount sufficient to modulate the desired response. As defined herein, a therapeutically effective
25 amount of protein or polypeptide (i.e., an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight.

30 The skilled artisan will appreciate that certain factors may influence the dosage required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject

with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments. In a preferred example, a subject is treated with antibody, protein, or polypeptide in the range of between about 0.1 to 20 mg/kg body weight, one time per week for
5 between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks. It will also be appreciated that the effective dosage of antibody, protein, or polypeptide used for treatment may increase or decrease over the course of a particular treatment. Changes in dosage may result and become apparent from the
10 results of diagnostic assays as described herein.

The present invention encompasses agents which modulate expression or activity. An agent may, for example, be a small molecule. For example, such small molecules include, but are not limited to, peptides, peptidomimetics, amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides,
15 nucleotide analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic
20 compounds having a molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

It is understood that appropriate doses of small molecule agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of the small molecule will vary, for
25 example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the small molecule to have upon the nucleic acid or polypeptide of the invention. Exemplary doses include milligram or microgram amounts of the small molecule per kilogram
30 of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is furthermore understood that appropriate doses of a

small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. Such appropriate doses may be determined using the assays described herein. When one or more of these small molecules is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes, or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF; Parsippany, NJ), or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be

fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, 5 polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion, and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various 10 antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride, in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an 15 agent that delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., an IL-9/IL-2 receptor-like protein or anti-IL-9/IL-2 receptor-like antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered 20 sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying, which yields a powder of the 25 active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be 30 incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding

agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth, or gelatin; an excipient such as starch or lactose, a
5 disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a
10 pressurized container or dispenser that contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally
15 known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art. The compounds can also be
20 prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery
25 systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions
30 (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated with each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. Depending on the type and severity of the disease, about 1 $\mu\text{g/kg}$ to about 15 mg/kg (e.g., 0.1 to 20 mg/kg) of antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 $\mu\text{g/kg}$ to about 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays. An exemplary dosing regimen is disclosed in WO 94/04188. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (*see, e.g., Chen et al. (1994) Proc. Natl. Acad. Sci. USA 91:3054-3057*). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

V. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (e.g., chromosomal mapping, tissue typing, forensic biology); (c) predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (e.g., therapeutic and prophylactic). The isolated nucleic acid molecules of the invention can be used to express IL-9/IL-2 receptor-like protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect IL-9/IL-2 receptor-like mRNA (e.g., in a biological sample) or a genetic lesion in an IL-9/IL-2 receptor-like gene, and to modulate IL-9/IL-2 receptor-like activity. In addition, the IL-9/IL-2 receptor-like proteins can be used to screen drugs or compounds that modulate the immune response as well as to treat disorders characterized by insufficient or excessive production of IL-9/IL-2 receptor-like protein or production of IL-9/IL-2 receptor-like protein forms that have decreased or aberrant activity compared to IL-9/IL-2 receptor-like wild type protein. In addition, the anti-IL-9/IL-2 receptor-like antibodies of the invention can be used to detect and isolate IL-9/IL-2 receptor-like proteins and modulate IL-9/IL-2 receptor-like activity.

A. Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules, or other drugs) that bind to IL-9/IL-2 receptor-like proteins or have a stimulatory or inhibitory effect on, for example, IL-9/IL-2 receptor-like expression or IL-9/IL-2 receptor-like activity.

The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including biological libraries, spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, nonpeptide

oligomer, or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (e.g., Houghten (1992) *Bio/Techniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (U.S. Patent No. 5,223,409), spores (U.S. Patent Nos. 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869), or phage (Scott and Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:6378-6382; and Felici (1991) *J. Mol. Biol.* 222:301-310).

Determining the ability of the test compound to bind to the IL-9/IL-2 receptor-like protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the IL-9/IL-2 receptor-like protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In a similar manner, one may determine the ability of the IL-9/IL-2 receptor-like protein to bind to or interact with an IL-9/IL-2 receptor-like target molecule. By "target molecule" is intended a molecule with which an IL-9/IL-2 receptor-like protein binds or interacts in nature. In a preferred embodiment, the ability of the IL-9/IL-2 receptor-like protein to bind to or interact with an IL-9/IL-2 receptor-like target molecule can be determined by monitoring the activity of the

target molecule. For example, the activity of the target molecule can be monitored by detecting induction of a cellular second messenger of the target (e.g., intracellular Ca^{2+} , diacylglycerol, IP3, etc.), detecting catalytic/enzymatic activity of the target on an appropriate substrate, detecting the induction of a reporter gene (e.g., an IL-9/IL-2 receptor-like-responsive regulatory element operably linked to a
5 nucleic acid encoding a detectable marker, e.g. luciferase), or detecting a cellular response, for example, cellular differentiation or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting an IL-9/IL-2 receptor-like protein or biologically
10 active portion thereof with a test compound and determining the ability of the test compound to bind to the IL-9/IL-2 receptor-like protein or biologically active portion thereof. Binding of the test compound to the IL-9/IL-2 receptor-like protein can be determined either directly or indirectly as described above. In a preferred embodiment, the assay includes contacting the IL-9/IL-2 receptor-like
15 protein or biologically active portion thereof with a known compound that binds IL-9/IL-2 receptor-like protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to preferentially bind to IL-9/IL-2 receptor-like protein or biologically active portion thereof as compared to the known compound.

20 In another embodiment, an assay is a cell-free assay comprising contacting IL-9/IL-2 receptor-like protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the IL-9/IL-2 receptor-like protein or biologically active portion thereof. Determining the ability of the test compound to
25 modulate the activity of an IL-9/IL-2 receptor-like protein can be accomplished, for example, by determining the ability of the IL-9/IL-2 receptor-like protein to bind to an IL-9/IL-2 receptor-like target molecule as described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of an IL-9/IL-2 receptor-like protein
30 can be accomplished by determining the ability of the IL-9/IL-2 receptor-like protein to further modulate an IL-9/IL-2 receptor-like target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the IL-9/IL-2 receptor-like protein or biologically active portion thereof with a known compound that binds an IL-9/IL-2 receptor-like protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to preferentially bind to or modulate the activity of an IL-9/IL-2 receptor-like target molecule.

In the above-mentioned assays, it may be desirable to immobilize either an IL-9/IL-2 receptor-like protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/IL-9/IL-2 receptor-like fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione-derivatized microtitre plates, which are then combined with the test compound or the test compound and either the nonadsorbed target protein or IL-9/IL-2 receptor-like protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtitre plate wells are washed to remove any unbound components and complex formation is measured either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of IL-9/IL-2 receptor-like binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either IL-9/IL-2 receptor-like protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated IL-9/IL-2 receptor-like molecules or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96-well plates (Pierce Chemicals). Alternatively, antibodies reactive with an IL-9/IL-2 receptor-like protein or target molecules but which do not interfere with binding of the IL-9/IL-2 receptor-like protein to its target molecule can be derivatized to the wells of

the plate, and unbound target or IL-9/IL-2 receptor-like protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the IL-9/IL-2
5 receptor-like protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the IL-9/IL-2 receptor-like protein or target molecule.

In another embodiment, modulators of IL-9/IL-2 receptor-like expression are identified in a method in which a cell is contacted with a candidate compound
10 and the expression of IL-9/IL-2 receptor-like mRNA or protein in the cell is determined relative to expression of IL-9/IL-2 receptor-like mRNA or protein in a cell in the absence of the candidate compound. When expression is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of IL-9/IL-2
15 receptor-like mRNA or protein expression. Alternatively, when expression is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of IL-9/IL-2 receptor-like mRNA or protein expression. The level of IL-9/IL-2 receptor-like mRNA or protein expression in the cells can be determined by methods described
20 herein for detecting IL-9/IL-2 receptor-like mRNA or protein.

In yet another aspect of the invention, the IL-9/IL-2 receptor-like proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (*see, e.g.,* U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Bio/Techniques*
25 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and PCT Publication No. WO 94/10300), to identify other proteins, which bind to or interact with IL-9/IL-2 receptor-like protein ("IL-9/IL-2 receptor-like-binding proteins" or "IL-9/IL-2 receptor-like-bp") and modulate IL-9/IL-2 receptor-like activity. Such IL-9/IL-2 receptor-like-binding proteins are also likely to be involved in the
30 propagation of signals by the IL-9/IL-2 receptor-like proteins as, for example, upstream or downstream elements of the IL-9/IL-2 receptor-like pathway.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

B. Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (1) map their respective genes on a chromosome; (2) identify an individual from a minute biological sample (tissue typing); and (3) aid in forensic identification of a biological sample. These applications are described in the subsections below.

10 1. Chromosome Mapping

The isolated IL-9/IL-2 receptor-like gene sequences of the invention can be used to map their respective IL-9/IL-2 receptor-like genes on a chromosome, thereby facilitating the location of gene regions associated with genetic disease. Computer analysis of IL-9/IL-2 receptor-like sequences can be used to rapidly select PCR primers (preferably 15-25 bp in length) that do not span more than one exon in the genomic DNA, thereby simplifying the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the IL-9/IL-2 receptor-like sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (e.g., human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow (because they lack a particular enzyme), but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes (D'Eustachio *et al.* (1983) *Science* 220:919-924). Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

Other mapping strategies that can similarly be used to map an IL-9/IL-2 receptor-like sequence to its chromosome include *in situ* hybridization (described in Fan *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:6223-27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization to
5 chromosome specific cDNA libraries. Furthermore, fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. For a review of this technique, see Verma *et al.* (1988) *Human Chromosomes: A Manual of Basic Techniques* (Pergamon Press, NY). The FISH technique can be used with a DNA
10 sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases will suffice to get good results in a reasonable amount of time.

15 Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene
20 families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Another strategy to map the chromosomal location of IL-9/IL-2 receptor-like genes uses IL-9/IL-2 receptor -like polypeptides and fragments and sequences of the present invention and antibodies specific thereto. This mapping can be
25 carried out by specifically detecting the presence of a IL-9/IL-2 receptor -like polypeptide in members of a panel of somatic cell hybrids between cells of a first species of animal from which the protein originates and cells from a second species of animal, and then determining which somatic cell hybrid(s) expresses the polypeptide and noting the chromosomes(s) from the first species of animal that it
30 contains. For examples of this technique, see Pajunen *et al.* (1988) *Cytogenet. Cell. Genet.* 47:37-41 and Van Keuren *et al.* (1986) *Hum. Genet.* 74:34-40. Alternatively, the presence of a IL-9/IL-2 receptor -like polypeptide in the somatic cell hybrids can be determined by assaying an activity or property of the

polypeptide, for example, enzymatic activity, as described in Bordelon-Riser *et al.* (1979) *Somatic Cell Genetics* 5:597-613 and Owerbach *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:5640-5644.

5 Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man*, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-
10 inheritance of physically adjacent genes), described in, e.g., Egeland *et al.* (1987) *Nature* 325:783-787.

 Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the IL-9/IL-2 receptor-like gene can be determined. If a mutation is observed in some or all of the affected individuals
15 but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete
20 sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

2. Tissue Typing

 The IL-9/IL-2 receptor-like sequences of the present invention can also be
25 used to identify individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes and probed on a Southern blot to yield unique bands for identification. The sequences
30 of the present invention are useful as additional DNA markers for RFLP (described in U.S. Patent 5,272,057).

 Furthermore, the sequences of the present invention can be used to provide an alternative technique for determining the actual base-by-base DNA sequence of

selected portions of an individual's genome. Thus, the IL-9/IL-2 receptor-like sequences of the invention can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

5 Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The IL-9/IL-2* receptor-like sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these
10 sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. The noncoding sequences of SEQ ID NO:1 or 3 can
15 comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If a predicted coding sequence, such as that in SEQ ID NO:1 or 3, is used, a more appropriate number of primers for positive individual identification would be 500 to 2,000.

20

3. Use of Partial IL-9/IL-2 Receptor-like Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. In this manner, PCR technology can be used to amplify DNA sequences taken
25 from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide
30 polynucleotide reagents, e.g., PCR primers, targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" that is unique to a particular individual. As mentioned above, actual base sequence information can

be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NO:1 or 3 are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the IL-9/IL-2 receptor-like sequences or portions thereof, e.g., fragments derived from the noncoding regions of SEQ ID NO:1 or 3 having a length of at least 20 or 30 bases.

The IL-9/IL-2 receptor-like sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes that can be used in, for example, an *in situ* hybridization technique, to identify a specific tissue. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such IL-9/IL-2 receptor-like probes, can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, e.g., IL-9/IL-2 receptor-like primers or probes can be used to screen tissue culture for contamination (i.e., screen for the presence of a mixture of different types of cells in a culture).

C. Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. These applications are described in the subsections below.

1. Diagnostic Assays

One aspect of the present invention relates to diagnostic assays for detecting IL-9/IL-2 receptor-like protein and/or nucleic acid expression as well as IL-9/IL-2 receptor-like activity, in the context of a biological sample. An exemplary method for detecting the presence or absence of IL-9/IL-2 receptor-like proteins in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting IL-9/IL-2 receptor-like protein or nucleic acid (e.g., mRNA, genomic

DNA) that encodes IL-9/IL-2 receptor-like protein such that the presence of IL-9/IL-2 receptor-like protein is detected in the biological sample. Results obtained with a biological sample from the test subject may be compared to results obtained with a biological sample from a control subject.

5 A preferred agent for detecting IL-9/IL-2 receptor-like mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to IL-9/IL-2 receptor-like mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length IL-9/IL-2 receptor-like nucleic acid, such as the nucleic acid of SEQ ID NO:1 or 3, or a portion thereof, such as a nucleic acid molecule of at least 15, 30,
10 50, 100, 250, or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to IL-9/IL-2 receptor-like mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

A preferred agent for detecting IL-9/IL-2 receptor-like protein is an
15 antibody capable of binding to IL-9/IL-2 receptor-like protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically
20 linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

25 The term "biological sample" is intended to include tissues, cells, and biological fluids isolated from a subject, as well as tissues, cells, and fluids present within a subject. That is, the detection method of the invention can be used to detect IL-9/IL-2 receptor-like mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of
30 IL-9/IL-2 receptor-like mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of IL-9/IL-2 receptor-like protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection

of IL-9/IL-2 receptor-like genomic DNA include Southern hybridizations.

Furthermore, *in vivo* techniques for detection of IL-9/IL-2 receptor-like protein include introducing into a subject a labeled anti-IL-9/IL-2 receptor-like antibody.

For example, the antibody can be labeled with a radioactive marker whose
5 presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional
10 means from a subject.

The invention also encompasses kits for detecting the presence of IL-9/IL-2 receptor-like proteins in a biological sample (a test sample). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing a disorder associated with aberrant expression of IL-9/IL-2 receptor-like protein
15 (e.g., an immunological disorder). For example, the kit can comprise a labeled compound or agent capable of detecting IL-9/IL-2 receptor-like protein or mRNA in a biological sample and means for determining the amount of an IL-9/IL-2 receptor-like protein in the sample (e.g., an anti-IL-9/IL-2 receptor-like antibody or an oligonucleotide probe that binds to DNA encoding an IL-9/IL-2 receptor-like
20 protein, e.g., SEQ ID NO:1 or 3). Kits can also include instructions for observing that the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of IL-9/IL-2 receptor-like sequences if the amount of IL-9/IL-2 receptor-like protein or mRNA is above or below a normal level.

25 For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) that binds to IL-9/IL-2 receptor-like protein; and, optionally, (2) a second, different antibody that binds to IL-9/IL-2 receptor-like protein or the first antibody and is conjugated to a detectable agent. For oligonucleotide-based kits, the kit can comprise, for example: (1) an
30 oligonucleotide, e.g., a detectably labeled oligonucleotide, that hybridizes to an IL-9/IL-2 receptor-like nucleic acid sequence or (2) a pair of primers useful for amplifying an IL-9/IL-2 receptor-like nucleic acid molecule.

The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can also comprise components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples that can be assayed and
5 compared to the test sample contained. Each component of the kit is usually enclosed within an individual container, and all of the various containers are within a single package along with instructions for observing whether the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of IL-9/IL-2 receptor-like proteins.

10

2. Other Diagnostic Assays

In another aspect, the invention features a method of analyzing a plurality of capture probes. The method can be used, e.g., to analyze gene expression. The method includes: providing a two dimensional array having a plurality of
15 addresses, each address of the plurality being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., a nucleic acid or peptide sequence; contacting the array with an IL-9/IL-2 receptor-like nucleic acid, preferably purified, polypeptide, preferably purified, or antibody, and thereby evaluating the plurality of capture
20 probes. Binding, e.g., in the case of a nucleic acid, hybridization, with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the IL-9/IL-2 receptor-like nucleic acid, polypeptide, or antibody. The capture probes can be a set of nucleic acids from a selected sample, e.g., a sample of nucleic acids derived from a control or non-stimulated tissue or cell.

25 The method can include contacting the IL-9/IL-2 receptor-like nucleic acid, polypeptide, or antibody with a first array having a plurality of capture probes and a second array having a different plurality of capture probes. The results of each hybridization can be compared, e.g., to analyze differences in expression between a first and second sample. The first plurality of capture probes can be from a control
30 sample, e.g., a wild type, normal, or non-diseased, non-stimulated, sample, e.g., a biological fluid, tissue, or cell sample. The second plurality of capture probes can be from an experimental sample, e.g., a mutant type, at risk, disease-state or disorder-state, or stimulated, sample, e.g., a biological fluid, tissue, or cell sample.

The plurality of capture probes can be a plurality of nucleic acid probes each of which specifically hybridizes, with an allele of an IL-9/IL-2 receptor-like sequence of the invention. Such methods can be used to diagnose a subject, e.g., to evaluate risk for a disease or disorder, to evaluate suitability of a selected treatment
5 for a subject, to evaluate whether a subject has a disease or disorder. Thus, for example, the h16445 sequence set forth in SEQ ID NO:1 encodes an IL-9/IL-2 receptor-like polypeptide that is associated with immune function, thus it is useful for evaluating immune disorders.

The method can be used to detect single nucleotide polymorphisms (SNPs),
10 as described below.

In another aspect, the invention features a method of analyzing a plurality of probes. The method is useful, e.g., for analyzing gene expression. The method includes: providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address
15 of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which express an IL-9/IL-2 receptor-like polypeptide of the invention or from a cell or subject in which an IL-9/IL-2 receptor-like-mediated response has been elicited, e.g., by contact of the cell with an IL-9/IL-2 receptor-like nucleic acid or protein of the invention, or administration to the cell or subject
20 an IL-9/IL-2 receptor-like nucleic acid or protein of the invention; contacting the array with one or more inquiry probes, wherein an inquiry probe can be a nucleic acid, polypeptide, or antibody (which is preferably other than an IL-9/IL-2 receptor-like nucleic acid, polypeptide, or antibody of the invention); providing a two dimensional array having a plurality of addresses, each address of the plurality
25 being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which does not express an IL-9/IL-2 receptor-like sequence of the invention (or does not express as highly as in the case of the IL-9/IL-2 receptor-like positive plurality of capture probes) or from a cell or
30 subject in which an IL-9/IL-2 receptor-like-mediated response has not been elicited (or has been elicited to a lesser extent than in the first sample); contacting the array with one or more inquiry probes (which is preferably other than an IL-9/IL-2 receptor-like nucleic acid, polypeptide, or antibody of the invention), and thereby

evaluating the plurality of capture probes. Binding, e.g., in the case of a nucleic acid, hybridization, with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the nucleic acid, polypeptide, or antibody.

5 In another aspect, the invention features a method of analyzing an IL-9/IL-2 receptor-like sequence of the invention, e.g., analyzing structure, function, or relatedness to other nucleic acid or amino acid sequences. The method includes: providing an IL-9/IL-2 receptor-like nucleic acid or amino acid sequence, e.g., the h16445 sequence set forth in SEQ ID NO:1 or a portion thereof; comparing the IL-
10 9/IL-2 receptor-like sequence with one or more preferably a plurality of sequences from a collection of sequences, e.g., a nucleic acid or protein sequence database; to thereby analyze the IL-9/IL-2 receptor-like sequence of the invention.

The method can include evaluating the sequence identity between an IL-9/IL-2 receptor-like sequence of the invention, e.g., the h16445 sequence, and a
15 database sequence. The method can be performed by accessing the database at a second site, e.g., over the internet.

In another aspect, the invention features, a set of oligonucleotides, useful, e.g., for identifying SNP's, or identifying specific alleles of an IL-9/IL-2 receptor-like sequence of the invention, e.g., the h16445 sequence. The set includes a
20 plurality of oligonucleotides, each of which has a different nucleotide at an interrogation position, e.g., an SNP or the site of a mutation. In a preferred embodiment, the oligonucleotides of the plurality identical in sequence with one another (except for differences in length). The oligonucleotides can be provided with differential labels, such that an oligonucleotides which hybridizes to one
25 allele provides a signal that is distinguishable from an oligonucleotides which hybridizes to a second allele.

3. Prognostic Assays

The methods described herein can furthermore be utilized as diagnostic or
30 prognostic assays to identify subjects having or at risk of developing a disease or disorder associated with IL-9/IL-2 receptor-like protein, IL-9/IL-2 receptor-like nucleic acid expression, or IL-9/IL-2 receptor-like activity. Prognostic assays can be used for prognostic or predictive purposes to thereby prophylactically treat an

individual prior to the onset of a disorder characterized by or associated with IL-9/IL-2 receptor-like protein, IL-9/IL-2 receptor-like nucleic acid expression, or IL-9/IL-2 receptor-like activity.

Thus, the present invention provides a method in which a test sample is
5 obtained from a subject, and IL-9/IL-2 receptor-like protein or nucleic acid (e.g., mRNA, genomic DNA) is detected, wherein the presence of IL-9/IL-2 receptor-like protein or nucleic acid is diagnostic for a subject having or at risk of
developing a disease or disorder associated with aberrant IL-9/IL-2 receptor-like expression or activity. As used herein, a "test sample" refers to a biological sample
10 obtained from a subject of interest. For example, a test sample can be a biological fluid (e.g., serum), cell sample, or tissue.

Furthermore, using the prognostic assays described herein, the present invention provides methods for determining whether a subject can be administered a specific agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide,
15 nucleic acid, small molecule, or other drug candidate) or class of agents (e.g., agents of a type that decrease IL-9/IL-2 receptor-like activity) to effectively treat a disease or disorder associated with aberrant IL-9/IL-2 receptor-like expression or activity. In this manner, a test sample is obtained and IL-9/IL-2 receptor-like protein or nucleic acid is detected. The presence of IL-9/IL-2 receptor-like protein
20 or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant IL-9/IL-2 receptor-like expression or activity.

The methods of the invention can also be used to detect genetic lesions or mutations in an IL-9/IL-2 receptor-like gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell
25 proliferation and/or differentiation. In preferred embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion or mutation characterized by at least one of an alteration affecting the integrity of a gene encoding an IL-9/IL-2 receptor-like-protein, or the misexpression of the IL-9/IL-2 receptor-like gene. For example, such genetic
30 lesions or mutations can be detected by ascertaining the existence of at least one of: (1) a deletion of one or more nucleotides from an IL-9/IL-2 receptor-like gene; (2) an addition of one or more nucleotides to an IL-9/IL-2 receptor-like gene; (3) a substitution of one or more nucleotides of an IL-9/IL-2 receptor-like gene; (4) a

chromosomal rearrangement of an IL-9/IL-2 receptor-like gene; (5) an alteration in the level of a messenger RNA transcript of an IL-9/IL-2 receptor-like gene; (6) an aberrant modification of an IL-9/IL-2 receptor-like gene, such as of the methylation pattern of the genomic DNA; (7) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an IL-9/IL-2 receptor-like gene; (8) a non-wild-type level of an IL-9/IL-2 receptor-like-protein; (9) an allelic loss of an IL-9/IL-2 receptor-like gene; and (10) an inappropriate post-translational modification of an IL-9/IL-2 receptor-like-protein. As described herein, there are a large number of assay techniques known in the art that can be used for detecting lesions in an IL-9/IL-2 receptor-like gene. Any cell type or tissue, preferably peripheral blood leukocytes, in which IL-9/IL-2 receptor-like proteins are expressed may be utilized in the prognostic assays described herein.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g., U.S. Patent Nos. 4,683,195 and 4,683,202*), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g., Landegran et al. (1988) Science 241:1077-1080; and Nakazawa et al. (1994) Proc. Natl. Acad. Sci. USA 91:360-364*), the latter of which can be particularly useful for detecting point mutations in the IL-9/IL-2 receptor-like-gene (*see, e.g., Abravaya et al. (1995) Nucleic Acids Res. 23:675-682*). It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include self sustained sequence replication (Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.* (1988) *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an IL-9/IL-2 receptor-like gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns of isolated test sample and control DNA digested with one or more

restriction endonucleases. Moreover, the use of sequence specific ribozymes (*see*, e.g., U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in an IL-9/IL-2 receptor-like molecule can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7:244-255; Kozal *et al.* (1996) *Nature Medicine* 2:753-759). In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the IL-9/IL-2 receptor-like gene and detect mutations by comparing the sequence of the sample IL-9/IL-2 receptor-like gene with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert ((1977) *Proc. Natl. Acad. Sci. USA* 74:560) or Sanger ((1977) *Proc. Natl. Acad. Sci. USA* 74:5463). It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays ((1995) *Bio/Techniques* 19:448), including sequencing by mass spectrometry (*see*, e.g., PCT Publication No. WO 94/16101; Cohen *et al.* (1996) *Adv. Chromatogr.* 36:127-162; and Griffin *et al.* (1993) *Appl. Biochem. Biotechnol.* 38:147-159).

Other methods for detecting mutations in the IL-9/IL-2 receptor-like gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). *See*, also Cotton *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4397; Saleeba *et al.* (1992) *Methods Enzymol.* 217:286-295. In a preferred embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more "DNA mismatch repair" enzymes that recognize mismatched base pairs in double-stranded DNA in defined systems for detecting and mapping point mutations in IL-9/IL-2 receptor-like cDNAs obtained from samples of cells. *See*, e.g., Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662. According to an exemplary embodiment, a probe based on an IL-9/IL-2 receptor-like sequence, e.g., a wild-type IL-9/IL-2 receptor-like sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair

enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, e.g., U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in IL-9/IL-2 receptor-like genes. For example, single-strand
5 conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild-type nucleic acids (Orita *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:2766; see also Cotton (1993) *Mutat. Res.* 285:125-144; Hayashi (1992) *Genet. Anal. Tech. Appl.* 9:73-79). The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the
10 secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double-stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.* (1991) *Trends Genet.* 7:5).

In yet another embodiment, the movement of mutant or wild-type
15 fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers *et al.* (1985) *Nature* 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further
20 embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) *Biophys. Chem.* 265:12753).

Examples of other techniques for detecting point mutations include, but are
25 not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found (Saiki *et al.* (1986) *Nature* 324:163); Saiki *et al.* (1989) *Proc. Natl. Acad. Sci. USA*
30 86:6230). Such allele-specific oligonucleotides are hybridized to PCR-amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele-specific amplification technology, which depends on selective PCR amplification, may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule so that amplification depends on
5 differential hybridization (Gibbs *et al.* (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition, it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini *et al.* (1992) *Mol. Cell*
10 *Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of
15 amplification.

The methods described herein may be performed, for example, by utilizing prepackaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, e.g., in clinical settings to
20 diagnosed patients exhibiting symptoms or family history of a disease or illness involving an IL-9/IL-2 receptor-like gene.

4. Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on IL-
25 9/IL-2 receptor-like activity (e.g., IL-9/IL-2 receptor-like gene expression) as identified by a screening assay described herein, can be administered to individuals to treat (prophylactically or therapeutically) disorders associated with aberrant IL-9/IL-2 receptor-like activity as well as to modulate the phenotype of an immune response. In conjunction with such treatment, the pharmacogenomics (i.e., the
30 study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the

pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (e.g., drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of IL-9/IL-2 receptor-like protein, expression of IL-9/IL-2 receptor-like nucleic acid, or mutation content of IL-9/IL-2 receptor-like genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. *See, e.g., Linder (1997) Clin. Chem. 43(2):254-266.* In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase deficiency (G6PD) is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (antimalarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

One pharmacogenomics approach to identifying genes that predict drug response, known as "a genome-wide association", relies primarily on a high-resolution map of the human genome consisting of already known gene-related markers (e.g., a "bi-allelic" gene marker map which consists of 60,000-100,000 polymorphic or variable sites on the human genome, each of which has two variants.) Such a high-resolution genetic map can be compared to a map of the genome of each of a statistically significant number of patients taking part in a Phase II/III drug trial to identify markers associated with a particular observed drug response or side effect. Alternatively, such a high resolution map can be generated from a combination of some ten-million known single nucleotide polymorphisms (SNPs) in the human genome. As used herein, an "SNP" is a common alteration that occurs in a single nucleotide base in a stretch of DNA. For example, a SNP may occur once per every 1000 bases of DNA. A SNP may be

involved in a disease process, however, the vast majority may not be disease-associated. Given a genetic map based on the occurrence of such SNPs, individuals can be grouped into genetic categories depending on a particular pattern of SNPs in their individual genome. In such a manner, treatment regimens
5 can be tailored to groups of genetically similar individuals, taking into account traits that may be common among such genetically similar individuals.

Alternatively, a method termed the "candidate gene approach", can be utilized to identify genes that predict drug response. According to this method, if a gene that encodes a drug's target is known (e.g., an IL-9/IL-2 receptor-like protein
10 of the present invention), all common variants of that gene can be fairly easily identified in the population and it can be determined if having one version of the gene versus another is associated with a particular drug response.

Alternatively, a method termed the "gene expression profiling", can be utilized to identify genes that predict drug response. For example, the gene
15 expression of an animal dosed with a drug (e.g., an IL-9/IL-2 receptor-like molecule or IL-9/IL-2 receptor-like modulator of the present invention) can give an indication whether gene pathways related to toxicity have been turned on.

Information generated from more than one of the above pharmacogenomics approaches can be used to determine appropriate dosage and treatment regimens
20 for prophylactic or therapeutic treatment of an individual. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an IL-9/IL-2 receptor-like molecule or IL-9/IL-2 receptor-like modulator of the invention, such as a modulator identified by one of the exemplary
25 screening assays described herein.

The present invention further provides methods for identifying new agents, or combinations, that are based on identifying agents that modulate the activity of one or more of the gene products encoded by one or more of the IL-9/IL-2 receptor-like genes of the present invention, wherein these products may be
30 associated with resistance of the cells to a therapeutic agent. Specifically, the activity of the proteins encoded by the IL-9/IL-2 receptor-like genes of the present invention can be used as a basis for identifying agents for overcoming agent resistance. By blocking the activity of one or more of the resistance proteins,

target cells, e.g., B-cells and colon cells, will become sensitive to treatment with an agent that the unmodified target cells were resistant to.

Monitoring the influence of agents (e.g., drugs) on the expression or activity of an IL-9/IL-2 receptor-like protein can be applied in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase IL-9/IL-2 receptor-like gene expression, protein levels, or upregulate IL-9/IL-2 receptor-like activity, can be monitored in clinical trials of subjects exhibiting decreased IL-9/IL-2 receptor-like gene expression, protein levels, or downregulated IL-9/IL-2 receptor-like activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease IL-9/IL-2 receptor-like gene expression, protein levels, or downregulate IL-9/IL-2 receptor-like activity, can be monitored in clinical trials of subjects exhibiting increased IL-9/IL-2 receptor-like gene expression, protein levels, or upregulated IL-9/IL-2 receptor-like activity. In such clinical trials, the expression or activity of an IL-9/IL-2 receptor-like gene, and preferably, other genes that have been implicated in, for example, an IL-9/IL-2 receptor-like-associated disorder can be used as a "read out" or markers of the phenotype of a particular cell.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called

ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of IL-9/IL-2 receptor-like protein, expression of IL-9/IL-2 receptor-like nucleic acid, or mutation content of IL-9/IL-2 receptor-like genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an IL-9/IL-2 receptor-like modulator, such as a modulator identified by one of the exemplary screening assays described herein.

5. Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of IL-9/IL-2 receptor-like genes (e.g., the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening but also in clinical trials. For example, the effectiveness of an agent, as determined by a screening assay as described herein, to increase or decrease IL-9/IL-2 receptor-like gene expression, protein levels, or protein activity, can be monitored in clinical trials of subjects exhibiting decreased or increased IL-9/IL-2 receptor-like gene expression, protein levels, or protein activity. In such clinical trials, IL-9/IL-2 receptor-like expression or activity and preferably that of other genes that have been implicated in for example, a cellular proliferation disorder, can be used as a marker of the immune responsiveness of a particular cell.

For example, and not by way of limitation, genes that are modulated in cells by treatment with an agent (e.g., compound, drug, or small molecule) that modulates IL-9/IL-2 receptor-like activity (e.g., as identified in a screening assay described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and

RNA prepared and analyzed for the levels of expression of IL-9/IL-2 receptor-like genes and other genes implicated in the disorder. The levels of gene expression (i.e., a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of IL-9/IL-2 receptor-like genes or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

10 In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (1) obtaining a preadministration sample from a subject
15 prior to administration of the agent; (2) detecting the level of expression of an IL-9/IL-2 receptor-like protein, mRNA, or genomic DNA in the preadministration sample; (3) obtaining one or more postadministration samples from the subject; (4) detecting the level of expression or activity of the IL-9/IL-2 receptor-like protein, mRNA, or genomic DNA in the postadministration samples; (5) comparing the
20 level of expression or activity of the IL-9/IL-2 receptor-like protein, mRNA, or genomic DNA in the preadministration sample with the IL-9/IL-2 receptor-like protein, mRNA, or genomic DNA in the postadministration sample or samples; and (vi) altering the administration of the agent to the subject accordingly to bring about the desired effect, i.e., for example, an increase or a decrease in the
25 expression or activity of an IL-9/IL-2 receptor-like protein.

C. Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a
30 disorder associated with aberrant IL-9/IL-2 receptor-like expression or activity. Additionally, the compositions of the invention find use in modulating the T-lymphocyte response. Thus, therapies for immune and respiratory disorders are encompassed herein.

1. Prophylactic Methods

In one aspect, the invention provides a method for preventing in a subject a disease or condition associated with an aberrant IL-9/IL-2 receptor-like expression or activity by administering to the subject an agent that modulates IL-9/IL-2 receptor-like expression or at least one IL-9/IL-2 receptor-like gene activity. Subjects at risk for a disease that is caused, or contributed to, by aberrant IL-9/IL-2 receptor-like expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein.

Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the IL-9/IL-2 receptor-like aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of IL-9/IL-2 receptor-like aberrancy, for example, an IL-9/IL-2 receptor-like agonist or IL-9/IL-2 receptor-like antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

2. Therapeutic Methods

Another aspect of the invention pertains to methods of modulating IL-9/IL-2 receptor-like expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of IL-9/IL-2 receptor-like protein activity associated with the cell. An agent that modulates IL-9/IL-2 receptor-like protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an IL-9/IL-2 receptor-like protein, a peptide, an IL-9/IL-2 receptor-like peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more of the biological activities of IL-9/IL-2 receptor-like protein. Examples of such stimulatory agents include active IL-9/IL-2 receptor-like protein and a nucleic acid molecule encoding an IL-9/IL-2 receptor-like protein that has been introduced into the cell. In another embodiment, the agent inhibits one or more of the biological activities of IL-9/IL-2 receptor-like protein. Examples of such inhibitory agents include antisense IL-9/IL-2 receptor-like nucleic acid molecules and anti-IL-9/IL-2 receptor-like antibodies.

These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an IL-9/IL-2 receptor-like protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or a combination of agents, that modulates (e.g., upregulates or downregulates) IL-9/IL-2 receptor-like expression or activity. In another embodiment, the method involves administering an IL-9/IL-2 receptor-like protein or nucleic acid molecule as therapy to compensate for reduced or aberrant IL-9/IL-2 receptor-like expression or activity.

Stimulation of IL-9/IL-2 receptor-like activity is desirable in situations in which an IL-9/IL-2 receptor-like protein is abnormally downregulated and/or in which increased IL-9/IL-2 receptor-like activity is likely to have a beneficial effect. Conversely, inhibition of IL-9/IL-2 receptor-like activity is desirable in situations in which IL-9/IL-2 receptor-like activity is abnormally upregulated and/or in which decreased IL-9/IL-2 receptor-like activity is likely to have a beneficial effect.

This invention is further illustrated by the following examples, which should not be construed as limiting.

EXPERIMENTAL

Example 1: Isolation of h16445 and m16445

Peripheral blood lymphocytes purified from heparinized blood of 22
5 normal donors depleted of B cells using anti-CD19 beads (Miltenyi Biotec, Inc.)
were combined in RPMI media containing 10% fetal bovine serum and incubated
at 37°C for 4, 14, and 24 hours. Harvested cells were pooled for RNA purification.
Poly-A+ RNA was converted to cDNA using oligo dT primers and reverse
transcriptase and cloned into pMET to generate a cDNA library. The average
10 insert size from this library was 1500 nucleotide base pairs. EST sequencing was
performed on this library, and greater than 10,000 sequences were subjected to
database analysis together with other proprietary sequences.

From this analysis, two distinct sequences, jthLa064e09t1 and
jthLa065b03t1, were combined into a single contiguous sequence and identified by
15 BLASTX sequence analysis to be similar to known cytokine receptors. No other
sequences were included in this contig. The highest blast hit at that time was SP
Accession No. Q01114 (SEQ ID NO:8), which codes for murine interleukin-9
receptor (IL-9R).

Clones corresponding to this single contiguous sequence were retrieved and
20 subjected to full sequence determination and reanalysis. This new sequence, while
still similar to the cytokine receptor family, did not appear to contain the entire
open reading frame for the protein. Primers designed from the 5' end of the
sequence were used to PCR-amplify sequences using RACE technology. These
clones were subjected to sequence determination and analysis, which revealed a
25 more extensive reading frame with further similarity to known cytokine receptors.
Upon further analysis, the clone h16445 was identified.

The identified clone h16445 encodes a transcript of approximately 2.3 Kb
(corresponding cDNA set forth in SEQ ID NO:1). The open reading frame (nt 349-
1965) of this transcript encodes a predicted 538 amino acid protein (SEQ ID NO:2)
30 having a molecular weight of approximately 59.1 kDa. A search of the nucleotide
and protein databases revealed that h16445 encodes a precursor polypeptide that
shares similarity with several cytokine receptor proteins. An alignment of the
protein sequences having highest similarity to the h16445 precursor polypeptide is

shown in Figure 1. The alignment was generated using the Clustal method with PAM250 residue weight table and sequence identities were determined by FASTA (Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448).

The h16445 protein displays similarity to the human IL-2 receptor beta chain (approximately 36.9% over a 130 amino acid overlap; SEQ ID NO:5; SP Accession Number P14784; Hatakeyama *et al.* (1989) *Science* 244(4904):551-556). It also displays similarity to the murine IL-2 receptor beta chain (approximately 32.7% identity over a 110 amino acid overlap; SEQ ID NO:6; SP Accession Number P16297; Kono *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87(5):1806-1810); the human IL-9 receptor (approximately 29.7% identity over a 158 amino acid overlap; SEQ ID NO:7; SP Accession Number Q01113; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694; Chang *et al.* (1994) *Blood* 83(11):3199-3205; Kermouni *et al.* (1995) *Genomics* 29(2):371-382); (approximately 28.3% identity over a 166 amino acid overlap) to the murine IL-9 receptor (SEQ ID NO:8; SP Accession Number Q01114; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694) (see Figure 1).

Using a similar database mining strategy, clone m16445 was identified from a three-week-old murine LTBM (long-term bone marrow cell) library made by stimulating the cells with heat-inactivated yeast hyphae at a hyphae:cell ratio of 2.3:1. The identified clone m16445 encodes a transcript of approximately 2.5 Kb (corresponding cDNA set forth in SEQ ID NO:3). The open reading frame (nt 391-1976) of this transcript encodes a predicted 529 amino acid protein (SEQ ID NO:4) having a molecular weight of approximately 58.3 kDa. This polypeptide represents a protein sequence encoded by the murine orthologue of the h16445 gene. An alignment of the m16445 protein with the h16445 protein reveals that these polypeptides share approximately 64.4% identity as determined by pairwise alignment (see Needleman and Wunsch (1970) *J. Mol. Biol.* 48:444).

Example 2: mRNA Expression and *In Situ* Expression of Clone h16445

A Northern blot analysis of h16445 revealed expression in a number of tissues, including the following, in order of highest to lowest expression: skeletal muscle, lymph node, thymus, spleen, brain, liver fibrosis, fetal liver, lung, and

liver, with skeletal muscle exhibiting an expression level about 20-fold higher than that exhibited by lymph node.

Expression of h16445 was measured by TaqMan[®] quantitative PCR (Perkin Elmer Applied Biosystems) in cDNA prepared from the following normal human
5 tissues: lymph node, spleen, thymus, brain, lung, skeletal muscle, fetal liver, and normal and fibrotic liver; the following primary cells: resting and phytohemagglutinin (PHA) activated peripheral blood mononuclear cells (PBMC); resting and PHA activated CD3⁺ cells, CD4⁺ and CD8⁺ T cells; Th1 and Th2 cells stimulated for six or 48 hours with anti-CD3 antibody; resting and
10 lipopolysaccharide (LPS) activated CD19⁺ B cells; CD34⁺ cells from mobilized peripheral blood (mPB CD34⁺), adult resting bone marrow (ABM CD34⁺), G-CSF mobilized bone marrow (mBM CD34⁺), and neonatal umbilical cord blood (CB CD34⁺); G-CSF mobilized peripheral blood leukocytes (mPB leukocytes); CD34⁻ cells purified from mPB leukocytes (mPB CD34⁻), adult resting bone marrow
15 (ABM CD34⁻), G-CSF mobilized bone marrow (mBM CD34⁻), and neonatal umbilical cord blood (CB CD34⁻); CD14⁺ cells; and granulocytes. Transformed human cell lines included K526, an erythroleukemia; HL60, an acute promyelocytic leukemia; Jurkat, a T cell leukemia; HEK 293, epithelial cells from embryonic kidney transformed with adenovirus 5 DNA; and Hep3B hepatocellular
20 liver carcinoma cells cultured in normal (HepB normal) or reduced oxygen tension (Hep3B hypoxia), or mock stimulated or stimulated with TGF- β .

Probes were designed by PrimerExpress software (PE Biosystems) based on the h16445 sequence. The h16445 sequence probe was labeled using FAM (6-carboxyfluorescein), and the β 2-microglobulin reference probe was labeled with a
25 different fluorescent dye, VIC. The differential labeling of the target sequence and internal reference gene thus enabled measurement in the same well. Forward and reverse primers and the probes for both β 2-microglobulin and the target h16445 sequence were added to the TaqMan[®] Universal PCR Master Mix (PE Applied Biosystems). Although the final concentration of primer and probe could vary,
30 each was internally consistent within a given experiment. A typical experiment contained 200 nM of forward and reverse primers plus 100 nM probe for β -2 microglobulin and 600 nM forward and reverse primers plus 200 nM probe for the target h16445 sequence. TaqMan[®] matrix experiments were carried out on an

ABI PRISM 7700 Sequence Detection System (PE Applied Biosystems). The thermal cycler conditions were as follows: hold for 2 min at 50°C and 10 min at 95°C, followed by two-step PCR for 40 cycles of 95°C for 15 sec followed by 60°C for 1 min.

5 The following method was used to quantitatively calculate h16445 expression in the various tissues relative to β -2 microglobulin expression in the same tissue. The threshold cycle (Ct) value is defined as the cycle at which a statistically significant increase in fluorescence is detected. A lower Ct value is indicative of a higher mRNA concentration. The Ct value of the h16445 sequence is normalized by subtracting the Ct value of the β -2 microglobulin gene to obtain a Δ Ct value using the following formula: Δ Ct = Ct_{h15571} - Ct _{β -2 microglobulin}. Expression is then calibrated against a cDNA sample showing a comparatively low level of expression of the h16445 sequence. The Δ Ct value for the calibrator sample is then subtracted from Δ Ct for each tissue sample according to the following formula:

10 $\Delta\Delta$ Ct = Δ Ct_{sample} - Δ Ct_{calibrator}. Relative expression is then calculated using the arithmetic formula given by $2^{-\Delta\Delta$ Ct}. Expression of the target h16445 sequence in each of the tissues tested was then graphically represented as discussed in more detail below.

Figure 2 shows expression of h16445 as determined in a broad panel of tissues and cell lines as described above, relative to expression in Hep3B hypoxia cells. The results indicate significant expression in HL60 and K562 cell lines, skeletal muscle, activated and resting B and CD8⁺ cells.

Expression of h16445 was also detected by *in situ* hybridization of riboprobes to cellular mRNAs in the following human tissues: spleen, tonsil, lymph node, and colon (normal and inflammatory bowel disease). Sense and anti-sense riboprobes (RNA transcripts) of cDNA encoding h16445 were generated using ³⁵S-dUTP, T3, and T7 polymerases, and standard *in vitro* transcription reaction reagents.

Six μ m sections of cryopreserved human tissue were prepared using a cryostat and annealed to glass slides, pre-hybed and hybridized to sense- and anti-sense h16445 riboprobes according to standard protocols. Slides containing hybridized tissues and riboprobes were washed extensively (according to standard procedures), dipped in NTB-2 photoemulsion, and were allowed to expose for two

5 weeks. Slides were developed and counter-stained with Hematoxylin and Eosin to assist in identifying different subtypes of leukocytes. Data were recorded as pictures of these tissue sections as visualized under a microscope using bright and dark fields. The data from two separate experiments are summarized in Tables I and II below.

10 High levels of h16445 expression were detected in tonsil and thymus tissue. Tissue from normal and diseased colon (inflammatory bowel disease (IBD)), and some diseased synovium (rheumatoid arthritis) was shown to express intermediate levels of h16445. Very low to no expression of h16445 was detected in tissue from lymph nodes. No expression of h16445 was detected in spleen or normal synovium and some diseased synovium tissues (osteoarthritis).

Table 1. Expression Analysis of Human 16445 by *In Situ* Hybridization

Tissue	16445	Comments
Tonsil (PIT202)	++	Expression in follicles, high in germinal center, low in corona. No expression in interfollicular areas.
Tonsil (PIT221)	++	Expression in follicles, high in germinal center, low in corona. No expression in interfollicular areas.
Normal Colon (NDR39)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
IBD (WUM02)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
IBD (WUM04)	+	Expression in follicles, high in germinal center, low in corona. . No expression in lamina propria. High background in eosinophils.
IBD (WUM06)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
Spleen (PIT268)	-	No expression.
Lymph Node (CLN484)	-	No expression of 16445. High expression of beta-actin.
Lymph Node (CLN820)	-	No expression of 16445. High expression of beta-actin.

Table II. Expression Analysis of Human 16445 by *In Situ* Hybridization

Tissue	16445	Comments
Tonsil (PIT222)	++	High expression in germinal centers and intermediate expression in medulla. No expression in interfollicular areas.
IBD (WUM2)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
IBD (WUM4)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
IBD (WUM6)	+	Expression in follicles, high in germinal center, low in corona. No expression in lamina propria. High background in eosinophils.
Thymus (BWH5)	++	No expression in cortex (immature thymocytes) and intermediate level of expression in the medulla, (mature thymocytes, although macrophages and dendritic cells also exist in medulla).
Lymph Node (CLN484)	+	Low expression in a small percentage (1%) of mononuclear cells in follicles.
Normal Synovium (NDR738a)	-	Very clean – virtually no infiltrate.
OA Synovium (NDR740c)	-	Extremely small sample – virtually no infiltrate.
RA Synovium (NEB02)	+	Low expression by a minority of mononuclear leukocytes in synovium.
RA Synovium (NEB03)	+	Low expression by a minority of mononuclear leukocytes in synovium.
RA Synovium (NEB04)	+/-	Little infiltrate in this sample. Interpretation difficult due to particulate matter.

Example 3: Functional Analysis of Human 16445 Signal Transduction

Amino acid sequence comparisons suggest that h16445 is a member of the hematopoietic Type I cytokine receptor family. Included in this family are the IL-2 receptor gamma chain dependent receptors for the cytokines IL-2, IL-4, IL-7, IL-9, and IL-15. In addition, these receptor-ligand complexes utilize common signaling intermediates such as the JAK and STAT family of proteins.

The signaling of h16445 was investigated as described below. Human 16445 was ectopically expressed in the human hepatoma cell line, HepG2. In this approach, HepG2 cells were cotransfected with cDNA clones encoding cytokine receptor subunits and a chloramphenicol acetyl transferase (CAT)-reporter plasmid containing eight copies of the cytokine-inducible hemopoietin receptor response element (HRRE-CAT) (Zeigler *et al.* (1995) *Eur. J. Immunol.* 25:399 and Morella (1995) *JBC* 270:8298). The ability of the transfected cells to signal when treated with the appropriate cytokine is measured by increased CAT activity. In addition, a plasmid encoding STAT5 was added to provide adequate signaling through this intermediate.

To test the effect of h16445 expression on signal transduction through known cytokine receptors, cotransfections were performed with HRRE-CAT, STAT5, and each of the receptor subunits IL-2 β , IL-4 α , IL-9 α , IL-7 α or TSLPR. In the case of the IL-4 and IL-9 receptors, the IL-2 receptor gamma chain was also introduced into cells. The effect of h16445 expression on signal transduction by the above-mentioned cytokine receptors was measured as a difference between cytokine-stimulated CAT expression in the presence or absence of h16445. Cytokine-stimulated expression was measured in cells transfected with control plasmid, 0.2 μ g/ml h16445 plasmid, or 1.0 μ g/ml h16445 plasmid 24 hours subsequent to the addition of cytokine ligand (Figure 3A and 3B).

Receptor signaling by IL-7R and TSLPR was the most dramatically affected by h16445 expression (Figure 3A and 3B). In cells transfected with 1 μ g/ml h16445 plasmid, IL-7- and TSLP-induced CAT activity was reduced by approximately 95% relative to cells transfected with control plasmid. Signal transduction through the other cytokine/cytokine receptor pairs was affected to a lesser degree. Signaling through IL-9/IL-9R was reduced by about 90% and

signaling by IL-4/IL-4R was reduced by about 30%. Human 16445 expression had only a modest effect on signaling by the IL-2/IL-2R receptor pair.

An additional experiment was performed to determine if the cytoplasmic domain of h16445 can function as a hematopoietic Type I cytokine receptor, by producing a signal that induces a transcriptional event common to this family of receptors. In this experiment, a construct was prepared in which the cytoplasmic portion of h16445 was fused to the extracellular and transmembrane domains of the IL-9 receptor alpha chain. The resulting chimeric receptor construct was transfected into HepG2 cells alone or in combination with the IL-2 receptor gamma. Cytokine-induced CAT expression was measured as described above (Figure 4). Addition of IL-9 to cells transfected with the IL-9/h16445 receptor chimera and IL-2R γ resulted in a greater than 30-fold increase in CAT expression. These data demonstrate that the cytoplasmic domain of h16445 functions as a Type I cytokine receptor.

Example 4: Preparation of Monoclonal Antibodies Specific for h16445

An h16445-human IgG1Fc fusion construct consisting of the leader sequence from human CD5 plus the region coding for amino acids 1 to 234 of h16445 was prepared. Fusion protein was expressed from mammalian COS cells by transient transfection of the fusion construct using Lipofectamine (Gibco BRL) as per manufacture's instructions. Supernatants were harvested on day 3 and day 7. Fusion protein was purified using ProsepTM Protein G glass beads.

Balb/c mice were immunized with DNA encoding the fusion protein described above using gene gun delivery of DNA as described in Kilpatrick *et al.* (1998) *Hybridoma* 17(6). A serum titer could be detected against the h16445-human IgG1Fc fusion protein by ELISA (Enzyme Linked ImmunoSorbent Assay) using standard methodology (See Harlow and Lane, *Antibodies : A Laboratory Manual* (Cold Spring Harbor Laboratory Press); Coligan *et al.*, eds.; *Current Protocols in Immunology* (John Wiley & Sons).

Mice were boosted with h16445-hIgG1Fc fusion protein intravenously 4 days prior to harvesting of the spleens. Fusions were carried out using standard protocols. Spleen cells from one mouse were fused with SP2/0 myeloma cells using standard polyethylene glycol (PEG) protocol (Harlow and Lane, *Antibodies :*

A Laboratory Manual (Cold Spring Harbor Laboratory Press); Coligan et al., eds.,
Current Protocols in Immunology (John Wiley & Sons).

Hybridoma lines were screened for secretion of h16445-specific antibodies
5 using the following methods:

- 1) ELISA using plate bound h16445-human IgG1Fc or human IgG1 (Sigma).
- 2) Transient transfection of COS or HEK293 cells with a plasmid encoding amino
10 acids 1 to 234 of the extracellular domain of h16445 plus a His tag and the C
terminal signal sequence from human placental alkaline phosphatase (GPI
linker signal) or with control vector. Hybridoma supernatants were screened
by FACs analysis for binding to cell-surface expressed h16445-His.
- 3) Transient transfection of HEK293 cells with full-length h16445/pCDNA3.1
15 plasmid. Hybridoma supernatants were tested for their ability to bind to the
cell surface expressed full length h16445 by FACs analysis.
- 4) Hybridoma supernatants were ranked according to their affinity for solid phase
h16445 or human IgG1 using Biacore.

Screening of hybridoma cell lines by ELISA using the 16445-IgG1 fusion
20 protein identified 27 positive supernatants. Of these all but one were also positive
when screened by FACS analysis for binding to the GPI-linked h16445
extracellular domain expressed on COS cells. The cell lines were then similarly
tested for binding to full-length h16445 expressed in HEK293 cells. All but two of
these cell lines were also positive, although to a lesser degree than observed for
25 binding to GPI-linked h16445 extracellular domain expressed on COS cells.
Representative experiments for h16445-GPI transfected HEK293 cells (h16445-EC
HEK) and h16445 full-length transfected HEK293 cells (h16445-FL HEK) are
shown in Figure 5 (A-D). Relative fluorescence intensity exhibited by these
transfected cells tagged with particular hybridoma supernatants (peak 2) is shown
30 versus that exhibited by untransfected cells (represented by peak 1), which served
as a control in these experiments. Similar positive binding results were also
observed for the BiaCore analysis.

Hybridoma cell lines selected for their ability to secrete h16445 specific antibodies were cloned using ClonalCell™-HY Medium D (StemCell Technologies Inc) as per manufacturer's instructions.

5 Example 5: Phenotypic Analysis of h16445 Expression on Tonsillar Lymphocytes

10 Surgical specimens from tonsillectomy patients were manually dispersed in RPMI-1640 plus 0.5% BSA. Lymphocytes were purified by standard ficoll centrifugation using lymphoprep (Sigma). Nonspecific binding to Fc receptors was blocked using human Ig (Pharmingen). Cells were stained using supernatants from hybridomas secreting antibodies that recognized h16445-transfected HEK293 cells. 50 µL of each supernatant was incubated with 1×10^6 cells for 30 minutes on ice and then washed with RPMI-1640 plus 0.5% BSA. Cells were resuspended in RPMI-1640 plus 0.5% BSA containing PE labeled goat anti-mouse F(ab')₂ secondary antibody and incubated with cells for 30 minutes on ice and then washed
15 twice in RPMI-1640 plus 0.5% BSA. For the final staining step, cells were incubated in CyChrome conjugated mouse anti-hCD19 and FITC conjugated mouse anti-hCD3 for 20 minutes on ice. Binding was then quantified using standard three-color analysis with a FACScan (Becton Dickinson) flow cytometer.

20 Staining was observed for all antibody supernatants that were positive for h16445-transfected cells. All expression was restricted to the CD19+ population with very few cells staining the CD3+ population, indicating primary expression in the B-cell compartment. Data was then analyzed by gating on the CD19+ population and comparing to staining using a control supernatant. Representative staining for three of the h16445-specific supernatants is shown in Figure 6.

25 Expression of h16445 as detected by staining with the h16445-specific hybridoma supernatants (peak 2) is shown relative to that detected by staining with an irrelevant antibody supernatant specific for the chemokine neurotactin (Nt) (peak 1). Thus CD19 and h16445 staining were nearly coincident in this tissue sample. h16445 may thus represent a novel marker for B lymphocytes.

30

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the

same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by
5 the following claims.

INDICATIONS RELATING TO DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 4, line 2	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depository institution American Type Culture Collection	
Address of depository institution (including postal code and country) 10801 University Blvd. Manassas, VA 20110-2209 US	
Date of deposit 14 July 1999 (14.07.99)	Accession Number PTA-350
C. ADDITIONAL INDICATIONS (leave blank if not applicable)	
This information is continued on an additional sheet <input type="checkbox"/>	
Page 13, line 14; page 17, line 31; page 20, line 4; page 23, line 32; page 28, line 24; page 90, lines 8, 11, 16, 20, 23 and 27; page 91, lines 3, 7, 25, 28 and 32; page 92, lines 10, 22, 25, 28 and 32; page 93, line 8	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indicators are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - 5 a) a nucleic acid molecule comprising a nucleotide sequence which is at least 45% identical to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof;
 - 10 b) a nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof;
 - 15 c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350;
 - 20 d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or the polypeptide encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350; and
 - 25 e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions.
- 30 2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

- a) a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof; and
- b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.
3. The nucleic acid molecule of claim 1 further comprising vector nucleic acid sequences.
4. The nucleic acid molecule of claim 1 further comprising nucleic acid sequences encoding a heterologous polypeptide.
5. A host cell which contains the nucleic acid molecule of claim 1.
6. The host cell of claim 5 which is a mammalian host cell.
7. A nonhuman mammalian host cell containing the nucleic acid molecule of claim 1.
8. An isolated polypeptide selected from the group consisting of:
- (a) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350;
- b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the polypeptide is encoded by a nucleic acid molecule

which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions; and

- 5 c) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 45% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof.

9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

10. The polypeptide of claim 8 further comprising heterologous amino acid sequences.

15

11. An antibody which selectively binds to a polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

- 20 (a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

- 25 b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350; and

- 30 c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID

NO:3, or a complement thereof under stringent conditions; comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

5 13. The method of claim 12 wherein said polypeptide comprises the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

10 14. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

 a) contacting the sample with a compound which selectively binds to a polypeptide of claim 8; and

 b) determining whether the compound binds to the polypeptide in the
15 sample.

 15. The method of claim 14, wherein the compound which binds to the polypeptide is an antibody.

20 16. A kit comprising a compound which selectively binds to a polypeptide of claim 8 and instructions for use.

 17. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

25 a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and

 b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample.

30 18. The method of claim 17, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

19. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 and instructions for use.

20. A method for identifying a compound which binds to a polypeptide of claim 8 comprising the steps of:

- a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and
- b) determining whether the polypeptide binds to the test compound.

21. The method of claim 20, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detecting of test compound/polypeptide binding;
- b) detection of binding using a competition binding assay;
- c) detection of binding using an assay for IL-9/IL-2 receptor-like-mediated signal transduction.

22. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

23. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

- a) contacting a polypeptide of claim 8 with a test compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

FIGURE 1

h16445 pro	MPR-----GWAAPL-----LGLLLGCGM-----GCPDLVCYTDYLOTVICILEHMLHP-ST 46
m16445 pro	MRA-----GPVAAAL-----LGLLLHGAAL-----SCLDLCTCYTDYLOTVICILEHMLHP-ST 46
hIL-2 Rc beta pro	MNA-----PAPSMPLPLLLPLPLATW-----ASAANVGTQPTCCFYNSRANISCU-----WSQDG-AL 54
mIL-2 Rc beta pro	MAT-----TALPMSLSLYVFLALLATPN-----ASAANVGTQPTCCFYNSRANISCU-----WSQDG-AL 54
hIL-9 Rc pro	HGIORCINZOWPTLESZALRRDH-GTLLACICICTCVCLOSVTGEQGGQOKAGAPTCLESNEIYR-IDC-----HWSAPELGG 74
mIL-9 Rc pro	MALORCAEGWTLERVAVKQ-----VBNFLIYSWCVSGVCRGVSVPEOGGQOKAGAPTCLESNEIYR-IDC-----HWSAPELGG 74
h16445 pro	LTLTWO-DQYEEELKDAZATSCSLHRSKSAHNAATHTMTCTCHMDVPHF-----MADDFESVNIIT-----DQSGNYSQECGSPFLAE 116
m16445 pro	LSLTLWQ-DEYEEELKDAZATSCSLHRSKSAHNAATHTMTCTCHMDVPHF-----LSDEVIIVNVI-----DQSGNYSQECGSPFLAE 116
hIL-2 Rc beta pro	QDTSQVHAMPIISLOVVHVTTHRCNISMELIS-----QASHFER-HLEFEARTLSPGHTWEZAP-----LTLKQKQEMICUE-----TLTP 200
mIL-2 Rc beta pro	NVTTCVHAMPIISLOVVHVTTHRCNISMELIS-----QASHFER-HLEFEARTLSPGHTWEZAP-----LTLKQKQEMICUE-----TLTP 200
hIL-9 Rc pro	HKLDPSPDLQ-SNISSGHCILTWSIS-----PALEPNTTUSYELAFKKQEZAFWEQAQHRDHVIG-----VTLWILEAFELDP 216
mIL-9 Rc pro	HKLDPSPDLQ-SNISSGHCILTWSIS-----PALEPNTTUSYELAFKKQEZAFWEQAQHRDHVIG-----VTLWILEAFELDP 216
h16445 pro	DSSVELQVRAA-----PMGSSVQGTWSEHSDDVIFOTQSEELKEG-----MNPMLLLLL-LLVIVFIRAFMSLKT 257
m16445 pro	DSSVLOLQVRAA-----PMGSSVQGTWSEHSDDVIFOTQSEELKEG-----MNPMLLLLL-LLVIVFIRAFMSLKT 257
hIL-2 Rc beta pro	DTQVEFOVRVK-----FLQGEF-----TTSWSPSQPLAFERTKPAALORDTIF-----MLGULLVGLSGAPGFIILVYLLINC 267
mIL-2 Rc beta pro	STVEFOVRVK-----FLQGEF-----TTSWSPSQPLAFERTKPAALORDTIF-----MLGULLVGLSGAPGFIILVYLLINC 267
hIL-9 Rc pro	GSIHEARLRVOMATLEZ-----DDVVEEERT-TGWSPPSQPLAFERTKPAALORDTIF-----MLGULLVGLSGAPGFIILVYLLINC 267
mIL-9 Rc pro	GSIHEARLRVOMATLEZ-----DDVVEEERT-TGWSPPSQPLAFERTKPAALORDTIF-----MLGULLVGLSGAPGFIILVYLLINC 267
h16445 pro	HL-----LWRLWKIKWA-VPSPEPFHPLYKGCSDGDKWVGAPFTOSSLEGLPWSPEVPS-----TLEVYISCHPPSPSPAKRLQLT 332
m16445 pro	HL-----LWRLWKIKWA-VPSPEPFHPLYKGCSDGDKWVGAPFTOSSLEGLPWSPEVPS-----TLEVYISCHPPSPSPAKRLQLT 332
hIL-2 Rc beta pro	RNTGPM-LKRLVKCMTFDPSPFOLSEHGQDVQKMLSSPSSFGGLPAISPLEVLERD-KVTOLLOQDKVPE 345
mIL-2 Rc beta pro	RNTGPM-LKRLVKCMTFDPSPFOLSEHGQDVQKMLSSPSSFGGLPAISPLEVLERD-KVTOLLOQDKVPE 345
hIL-9 Rc pro	SP-----RVRIFYONVPSAMFOPLOYSVHNGFOITMGAHRAGVLLSDCAGTPQAGLE-----PCVQENTALTTCGPAFPW 367
mIL-9 Rc pro	SP-----RVRIFYONVPSAMFOPLOYSVHNGFOITMGAHRAGVLLSDCAGTPQAGLE-----PCVQENTALTTCGPAFPW 367
h16445 pro	ELQZPAELVESDGVKPSFW-----PIAONSGGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGYFALDL DAGLE 409
m16445 pro	ELQZPAELVESDGVKPSFW-----PIAONSGGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGYFALDL DAGLE 409
hIL-2 Rc beta pro	PASLSNHSLSLTCFTNCGYF-FPHLPDALEIEAC-----OVV-FTYDPSYEDPDQVAGAFIIGSEPOPLPLSGEDDAY 418
mIL-2 Rc beta pro	PPLSPSGHSGHSCFTNCGYF-FPHLPDALEIEAC-----OVV-FTYDPSYEDPDQVAGAFIIGSEPOPLPLSGEDDAY 418
hIL-9 Rc pro	KSVALEEEOEGPGTRLPCN-----LSEEDVLPAGCTEWRVOTLALYLPQ-----DWAPTSLTRAPPDSEGRSS 432
mIL-9 Rc pro	OFACLKWEATAPG-----FPGU-----POSEHVLPAAGCLLEGOESAYLPQ-----DWAPTSLTRAPPDSEGRSS 432
h16445 pro	PEPGLBEDPDL DAGTTVLSGCGVSAGCPGCGPLGSLIDRLKPPADGEE-----DMAAGLPMWGGGRSPGVSESEAGSPAGLDM 487
m16445 pro	SGPNSEEDLAVTDPAFLSCGCVSGLRLQGSPOSLLDRLLSLPAKEG-----DMTADPTHTGSPGGGSESEAGSPAGLDM 487
hIL-2 Rc beta pro	CTFPPSRDLDLLFSPSL-----GPPSPSTAPQSGAGE-ERMPESTQERVPRDMPO-PLGPTPGVPDLVDFQPPPELVLR 494
mIL-2 Rc beta pro	CAPPSPRDLDLLFSPSL-----GPPSPSTAPQSGAGE-ERMPESTQERVPRDMPO-PLGPTPGVPDLVDFQPPPELVLR 494
hIL-9 Rc pro	SSSSSSSN-----NNNYCALGC-----YGGWHLSALP-----GNTQSSGPIPALAC 471
mIL-9 Rc pro	SSSSSSSN-----SSDYCHLDC-----CEECHLSAP-----GNTQSSGPIPALAC 471
h16445 pro	DFDSDGFGVSDCLSPV ECDFTSPDQEGPPRSYLROWVVI PPP-----LSSPGPOAS----- 451
m16445 pro	DFDSDGFGVSDCLSPV ECDFTSPDQEGPPRSYLROWVVI PPP-----LSSPGPOAS----- 451
hIL-2 Rc beta pro	EA-GEVVPDAGPREGVSFHSFPQGGEPALNARLPLNTDAYSLSQELTQGGDPTHLV-----PVDSGAOSS----- 539
mIL-2 Rc beta pro	GD-GEGLSANSSEGA SVBEONLHGQDQDQGGPILTLNTDAYSLSQELTQGGDPTHLV-----PVDSGAOSS----- 539
hIL-9 Rc pro	G-LSCDHQGLLETQGVAMVLAGHCORPOLHEDLOMLLP SV-----LSKARSMTF----- 521
mIL-9 Rc pro	-----LTLAORVALPVEER-----LSKARSMTF----- 521

Decoration '!' : Side (with solid black) residues that match the consensus exactly.

FIGURE 2

h 16445 Expression

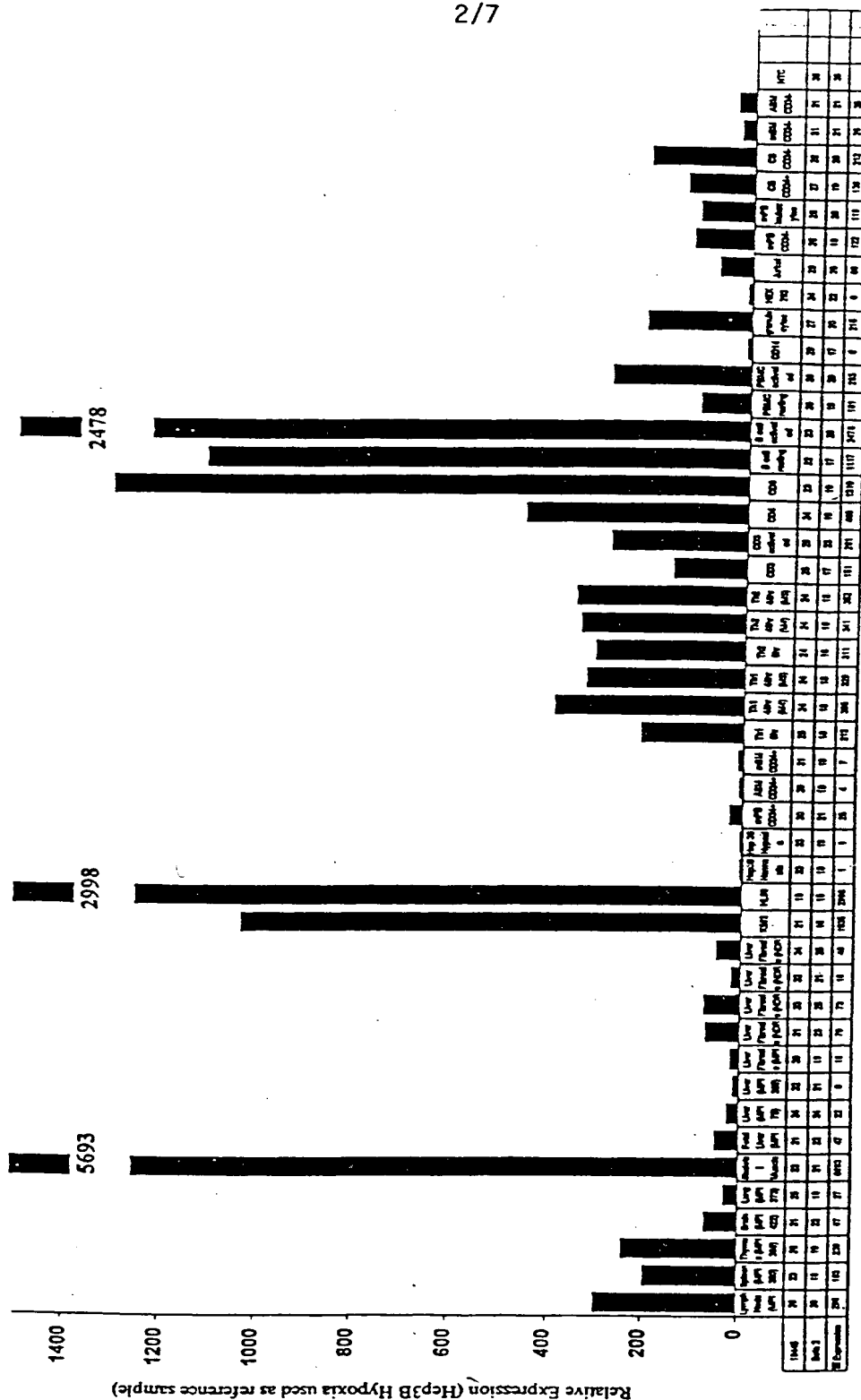


FIGURE 3A

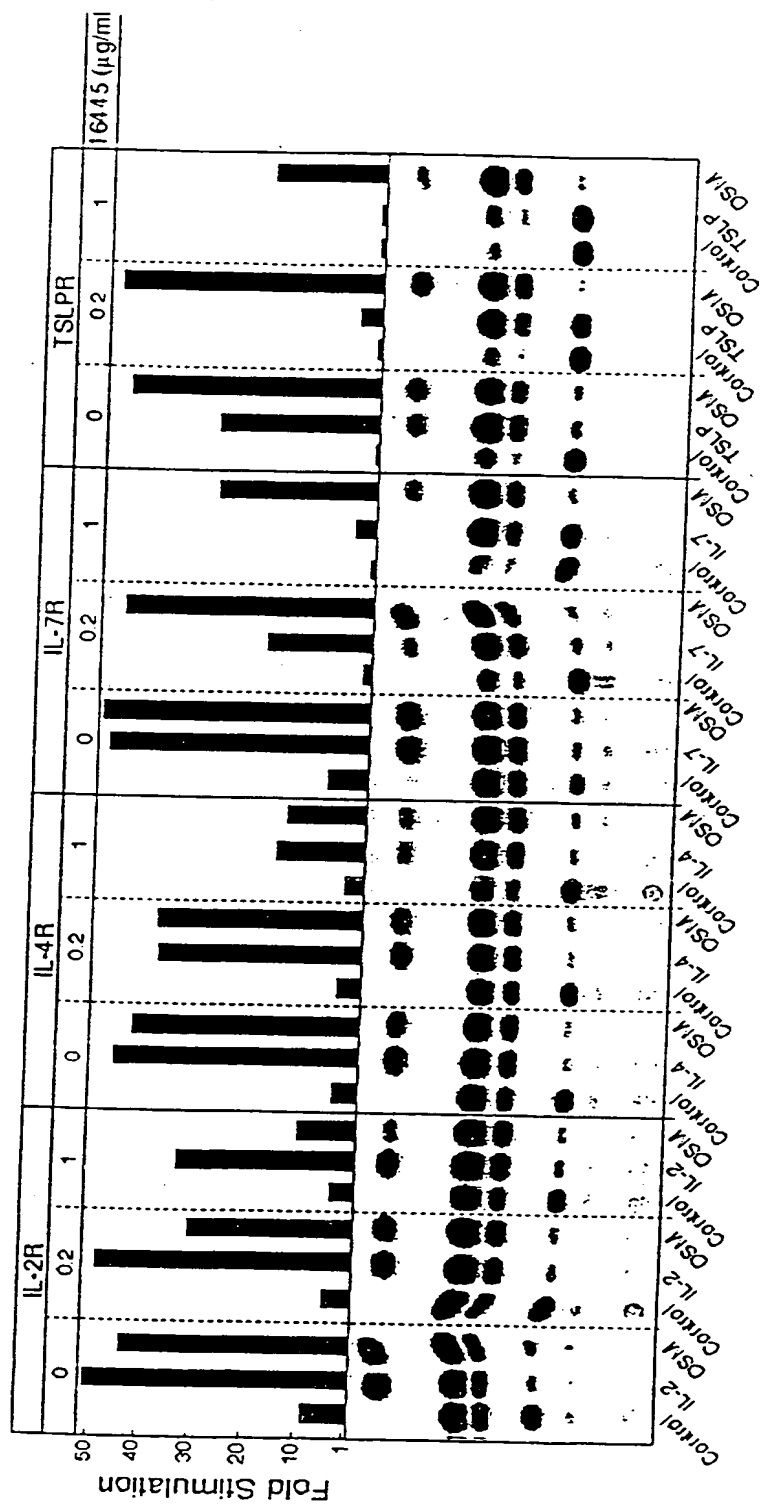


FIGURE 3B

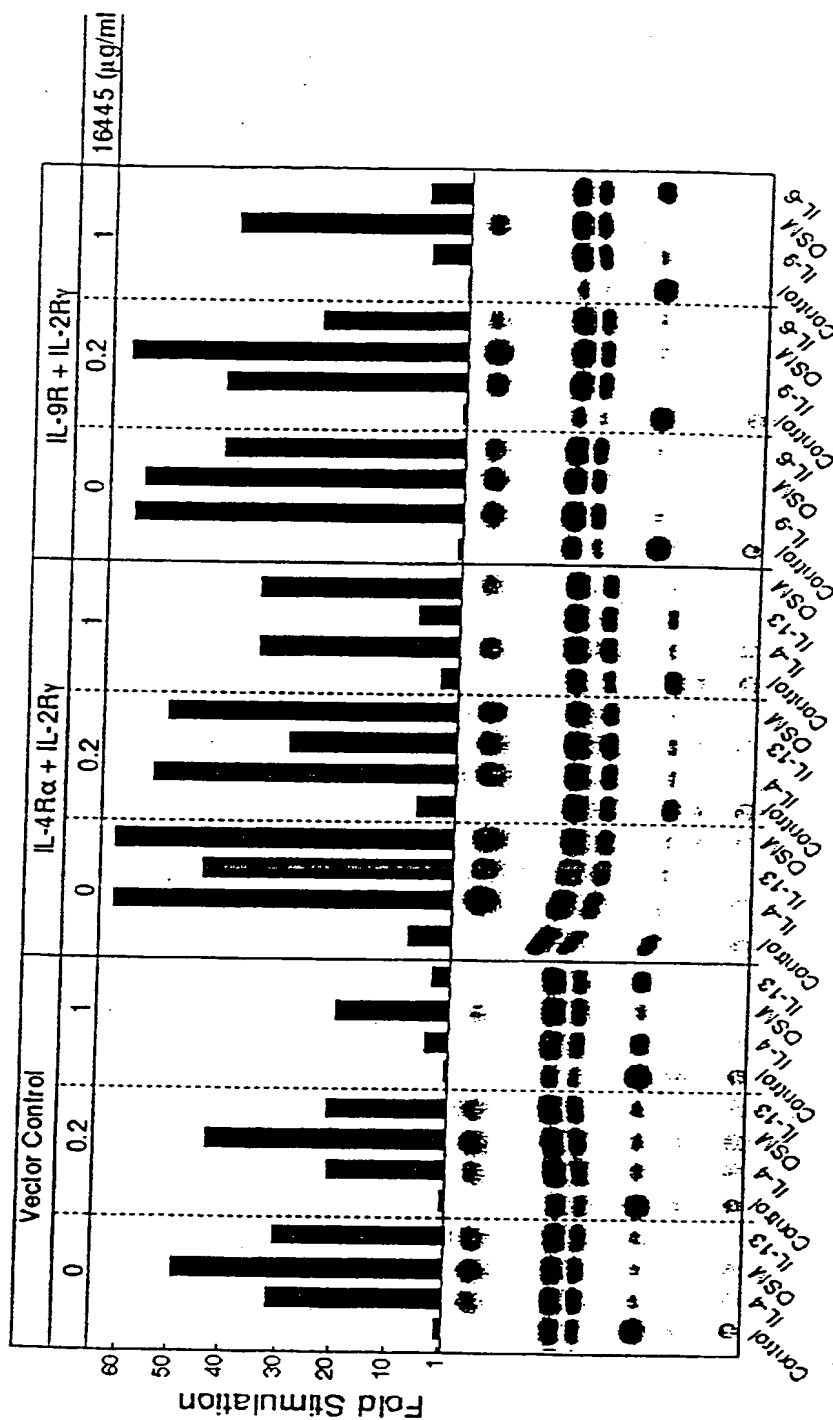


FIGURE 4

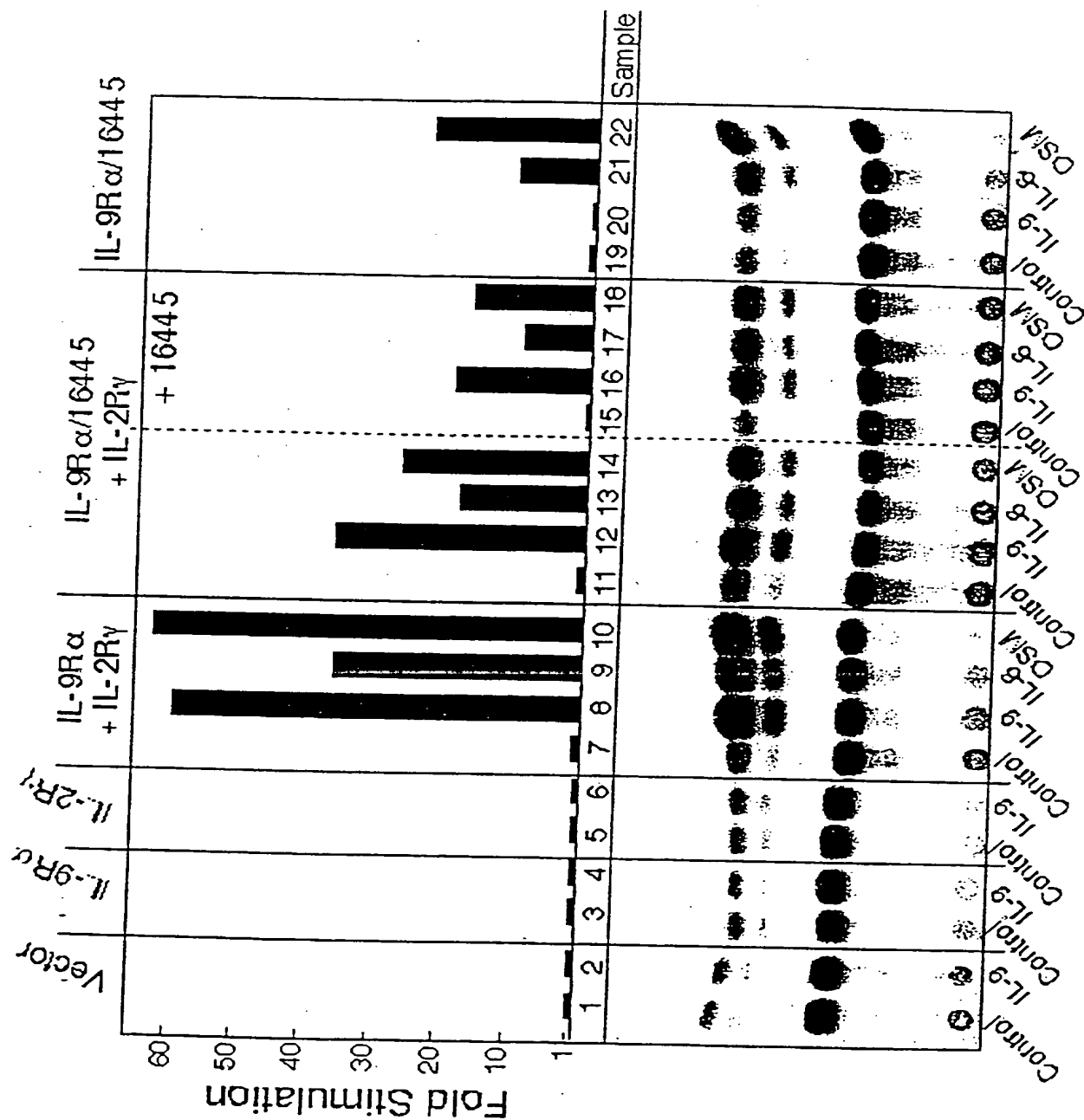


FIGURE 5

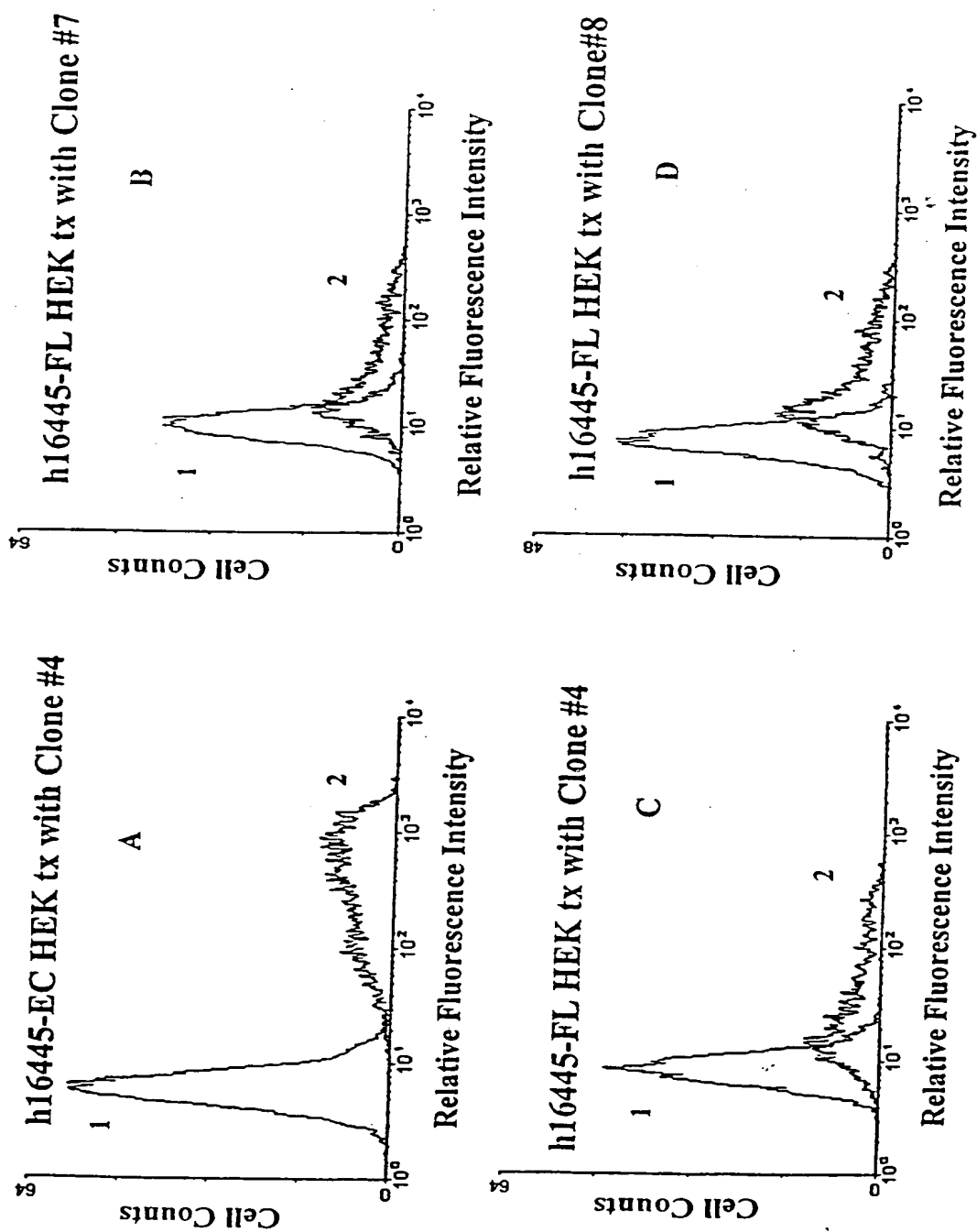
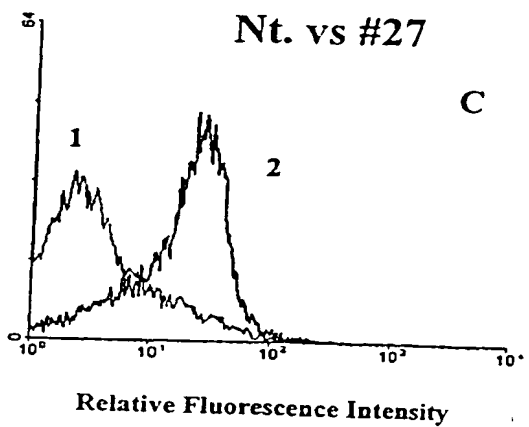
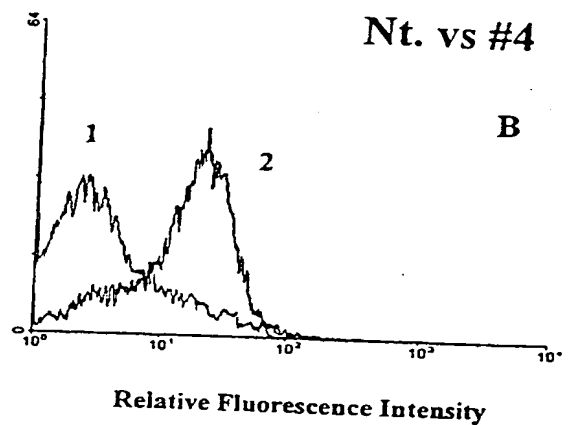
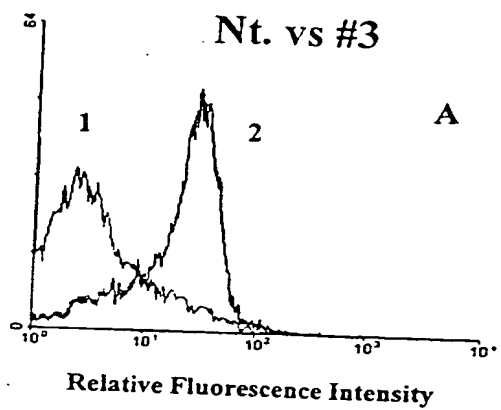


FIGURE 6



SEQUENCE LISTING

<110> Hodge, Martin R.

<120> Novel IL-9/IL-2 Receptor-Like Molecules
and Uses Thereof

<130> 5800-17A-1

<150> US 09/313,913

<151> 1999-05-18

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<221> CDS

<222> (349)...(1962)

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ggaggcccag ctgcccgtca tcagagtgtc aggtcttatg acagcctgat tggtgactcg      180
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atggatttct gagaaagaag ccgaaacaga aggcccgtag gagtcagc atg ccg cgt      357
                                         Met Pro Arg
                                         1

ggc tgg gcc gcc ccc ctg ctc ctg ctg ctg ctc cag gga ggc tgg ggc      405
Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly Gly Trp Gly
      5              10              15

tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc      453
Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
      20              25              30              35

atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg      501
Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
              40              45              50

caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc      549
Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
              55              60              65

cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg      597
His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
              70              75              80

gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca      645
Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
      85              90              95

gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct      693

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Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala	
100 105 110 115	
gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca	741
Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser	
120 125 130	
gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc	789
Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe	
135 140 145	
tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg	837
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg	
150 155 160	
gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac	885
Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp	
165 170 175	
tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc	933
Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser	
180 185 190 195	
tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag	981
Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln	
200 205 210	
ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca	1029
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser	
215 220 225	
gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc ctg	1077
Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu Leu	
230 235 240	
ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat cca	1125
Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His Pro	
245 250 255	
ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag cgg	1173
Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu Arg	
260 265 270 275	
ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa tgg	1221
Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys Trp	
280 285 290	
gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg agc	1269
Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp Ser	
295 300 305	
cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cca cgg	1317
Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro Arg	
310 315 320	
agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca gag	1365
Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala Glu	
325 330 335	
ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca gcc	1413
Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr Ala	

340	345	350	355	
cag aac tcg ggg ggc tca gct tac agt gag gag agg gat cgg cca tac				1461
Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr	360	365	370	
ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg cca				1509
Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro	375	380	385	
tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg gac				1557
Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp	390	395	400	
ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg				1605
Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu	405	410	415	
gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc agc				1653
Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser	420	425	430	435
cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca				1701
Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro	440	445	450	
ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc				1749
Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly	455	460	465	
cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg gcc				1797
Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu Ala	470	475	480	
ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac tgc				1845
Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys	485	490	495	
agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga ccc				1893
Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro	500	505	510	515
ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt tcg				1941
Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser	520	525	530	
agc cct gga ccc cag gcc agc taatgaggct gactggatgt ccagagctgg				1992
Ser Pro Gly Pro Gln Ala Ser	535			
ccaggccact gggccctgag ccagagacaa ggtaacctgg gctgtgatgt gaagacacct				2052
gcagcctttg gtctcctgga tgggcctttg agcctgatgt ttacagtgtc tgtgtgtgtg				2112
tgtgcatatg tgtgtgtgtg catatgcatg tgtgtgtgtg tgtgtgtctt aggtgcgcag				2172
tggcatgtcc acgtgtgtgt gtgattgcac gtgcctgtgg gcctgggata atgcccattg				2232
tactccatgc attcacctgc cctgtgcatg tctggactca cggagctcac ccatgtgcac				2292
aagtgtgcac agtaaacgtg tttgtggtca aaaaaaaaaa aaaaaaaaaa a				2343

<210> 2

<211> 538

<212> PRT

<213> Homo sapiens IL-2/IL-9 Receptor Like

<400> 2

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
 225 230 235 240
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 245 250 255
 Thr His Pro Leu Trp Arg Leu Trp Lys Ile Trp Ala Val Pro Ser
 260 265 270
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 275 280 285
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 290 295 300
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 305 310 315 320
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser

tcc tgg gac tca gct tat gac gaa ccc tcc aac tac gtg ctg aga ggc Ser Trp Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly 140 145 150	846
aag cta caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala 155 160 165	894
gtg agg ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct Val Arg Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser 170 175 180	942
ctt ctc cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag atg Leu Leu Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Met 185 190 195 200	990
cgg gca gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag Arg Ala Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu 205 210 215	1038
tgg agt gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala 220 225 230	1086
ggc tgg gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc Gly Trp Asp Pro His Met Leu Leu Leu Leu Ala Val Leu Ile Ile Val 235 240 245	1134
ctg gtt ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa Leu Val Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys 250 255 260	1182
aag ata tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg Lys Ile Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu 265 270 275 280	1230
tac agg gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc Tyr Arg Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe 285 290 295	1278
acg gcc tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca Thr Ala Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser 300 305 310	1326
gcc tta cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg Ala Leu His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly 315 320 325	1374
ctg ccg ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct Leu Pro Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro 330 335 340	1422
ggt cac tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc Gly His Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala 345 350 355 360	1470
tac agt gag gag aga gac cgg cca tat ggt ctg gtg tcc att gac aca Tyr Ser Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr 365 370 375	1518

gtg act gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt 1566
Val Thr Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys
380 385 390

gag gat gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct 1614
Glu Asp Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser
395 400 405

ggc cct aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg 1662
Gly Pro Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu
410 415 420

tct tgc ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca 1710
Ser Cys Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro
425 430 435 440

ggc agc cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac 1758
Gly Ser Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp
445 450 455

tgg aca gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct 1806
Trp Thr Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Gly Ser
460 465 470

gag agt gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac 1854
Glu Ser Glu Ala Gly Ser Pro Gly Leu Asp Met Asp Thr Phe Asp
475 480 485

agt ggc ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa 1902
Ser Gly Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu
490 495 500

gga ccc cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca 1950
Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro
505 510 515 520

cct gtg gac agt gga gcc cag agc agc tagcatataa taaccagcta 1997
Pro Val Asp Ser Gly Ala Gln Ser Ser
525

tagtgagaag aggcctctga gcctggcatt tacagtgtga acatgtaggg gtgtgtgtgt 2057
gtgtgtgtgt cttgggttgt gtgttagcac atccatgttg ggatttggtc tgttgctatg 2117
tattggaatg ctaaattctc taccctaaagt tctaggccta cgagtgaatt ctcatgttta 2177
caaacttgct gtgtaaacct tggtccttaa tttaatacca ttggttaaata aaaattggct 2237
gcaaccaatt actggagagg agaggagagg agaggagagg agaggagagg agaggctgcc 2297
gtgaggggag agggaccatg agcctgtggc caggagaaac agcaagtatc tggggtacac 2357
tggtgaggag gtggccaggc cagcagttag aagagtagat taggggtgac ctccagtatt 2417
tgtcaaagcc aattaaaata acaaaaaaaa aaaaaaagg 2456

<210> 4
<211> 529
<212> PRT
<213> Mus musculus

<400> 4
Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Leu Ile Leu His Gly
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Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr
20 25 30
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
35 40 45

Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe
 50 55 60
 Cys Ser Leu His Lys Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
 65 70 75 80
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val
 85 90 95
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val
 115 120 125
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu
 130 135 140
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 180 185 190
 Asp Ser Ser Tyr Gln Leu Gln Met Arg Ala Ala Pro Gln Pro Gly Thr
 195 200 205
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu
 225 230 235 240
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
 245 250 255
 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr
 260 265 270
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe
 275 280 285
 Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val
 290 295 300
 Pro Gln Ser Ser Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro
 305 310 315 320
 Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu
 325 330 335
 Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu
 340 345 350
 Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 355 360 365
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly
 370 375 380
 Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met
 385 390 395 400
 Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu
 405 410 415
 Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser
 420 425 430
 Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg
 435 440 445
 Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg
 450 455 460
 Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro
 465 470 475 480
 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys
 485 490 495
 Gly Ser Pro Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg
 500 505 510
 Gln Trp Val Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser
 515 520 525
 Ser

<210> 5
 <211> 551
 <212> PRT
 <213> Homo sapiens

<400> 5

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Met Ala Ala Pro Ala Leu Ser Trp Arg Leu Pro Leu Leu Ile Leu Leu
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Leu Pro Leu Ala Thr Ser Trp Ala Ser Ala Ala Val Asn Gly Thr Ser
20     25     30
Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp
35     40     45
Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp
50     55     60
Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser
65     70     75     80
Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln
85     90     95
Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu
100    105    110
Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu
115    120    125
Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu
130    135    140
Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr
145    150    155    160
Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His
165    170    175
Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp
180    185    190
Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val
195    200    205
Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser
210    215    220
Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Thr
225    230    235    240
Ile Pro Trp Leu Gly His Leu Leu Val Gly Leu Ser Gly Ala Phe Gly
245    250    255
Phe Ile Ile Leu Val Tyr Leu Leu Ile Asn Cys Arg Asn Thr Gly Pro
260    265    270
Trp Leu Lys Lys Val Leu Lys Cys Asn Thr Pro Asp Pro Ser Lys Phe
275    280    285
Phe Ser Gln Leu Ser Ser Glu His Gly Gly Asp Val Gln Lys Trp Leu
290    295    300
Ser Ser Pro Phe Pro Ser Ser Ser Phe Ser Pro Gly Gly Leu Ala Pro
305    310    315    320
Glu Ile Ser Pro Leu Glu Val Leu Glu Arg Asp Lys Val Thr Gln Leu
325    330    335
Leu Leu Gln Gln Asp Lys Val Pro Glu Pro Ala Ser Leu Ser Ser Asn
340    345    350
His Ser Leu Thr Ser Cys Phe Thr Asn Gln Gly Tyr Phe Phe Phe His
355    360    365
Leu Pro Asp Ala Leu Glu Ile Glu Ala Cys Gln Val Tyr Phe Thr Tyr
370    375    380
Asp Pro Tyr Ser Glu Glu Asp Pro Asp Glu Gly Val Ala Gly Ala Pro
385    390    395    400
Thr Gly Ser Ser Pro Gln Pro Leu Gln Pro Leu Ser Gly Glu Asp Asp
405    410    415
Ala Tyr Cys Thr Phe Pro Ser Arg Asp Asp Leu Leu Leu Phe Ser Pro

```


420 425 430
 Ser Leu Leu Gly Gly Pro Ser Pro Pro Ser Thr Ala Pro Gly Gly Ser
 435 440 445
 Gly Ala Gly Glu Glu Arg Met Pro Pro Ser Leu Gln Glu Arg Val Pro
 450 455 460
 Arg Asp Trp Asp Pro Gln Pro Leu Gly Pro Pro Thr Pro Gly Val Pro
 465 470 475 480
 Asp Leu Val Asp Phe Gln Pro Pro Pro Glu Leu Val Leu Arg Glu Ala
 485 490 495
 Gly Glu Glu Val Pro Asp Ala Gly Pro Arg Glu Gly Val Ser Phe Pro
 500 505 510
 Trp Ser Arg Pro Pro Gly Gln Gly Glu Phe Arg Ala Leu Asn Ala Arg
 515 520 525
 Leu Pro Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln Glu Leu Gln Gly
 530 535 540
 Gln Asp Pro Thr His Leu Val
 545 550

<210> 6
 <211> 539
 <212> PRT
 <213> Mus musculus

<400> 6
 Met Ala Thr Ile Ala Leu Pro Trp Ser Leu Ser Leu Tyr Val Phe Leu
 1 5 10 15
 Leu Leu Leu Ala Thr Pro Trp Ala Ser Ala Ala Val Lys Asn Cys Ser
 20 25 30
 His Leu Glu Cys Phe Tyr Asn Ser Arg Ala Asn Val Ser Cys Met Trp
 35 40 45
 Ser His Glu Glu Ala Leu Asn Val Thr Thr Cys His Val His Ala Lys
 50 55 60
 Ser Asn Leu Arg His Trp Asn Lys Thr Cys Glu Leu Thr Leu Val Arg
 65 70 75 80
 Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ser Phe Pro Glu Ser
 85 90 95
 Gln Ser Leu Thr Ser Val Asp Leu Leu Asp Ile Asn Val Val Cys Trp
 100 105 110
 Glu Glu Lys Gly Trp Arg Arg Val Lys Thr Cys Asp Phe His Pro Phe
 115 120 125
 Asp Asn Leu Arg Leu Val Ala Pro His Ser Leu Gln Val Leu His Ile
 130 135 140
 Asp Thr Gln Arg Cys Asn Ile Ser Trp Lys Val Ser Gln Val Ser His
 145 150 155 160
 Tyr Ile Glu Pro Tyr Leu Glu Phe Glu Ala Arg Arg Arg Leu Leu Gly
 165 170 175
 His Ser Trp Glu Asp Ala Ser Val Leu Ser Leu Lys Gln Arg Gln Gln
 180 185 190
 Trp Leu Phe Leu Glu Met Leu Ile Pro Ser Thr Ser Tyr Glu Val Gln
 195 200 205
 Val Arg Val Lys Ala Gln Arg Asn Asn Thr Gly Thr Trp Ser Pro Trp
 210 215 220
 Ser Gln Pro Leu Thr Phe Arg Thr Arg Pro Ala Asp Pro Met Lys Glu
 225 230 235 240
 Ile Leu Pro Met Ser Trp Leu Arg Tyr Leu Leu Leu Val Leu Gly Cys
 245 250 255
 Phe Ser Gly Phe Phe Ser Cys Val Tyr Ile Leu Val Lys Cys Arg Tyr
 260 265 270
 Leu Gly Pro Trp Leu Lys Thr Val Leu Lys Cys His Ile Pro Asp Pro
 275 280 285
 Ser Glu Phe Phe Ser Gln Leu Ser Ser Gln His Gly Gly Asp Leu Gln

290 295 300
 Lys Trp Leu Ser Ser Pro Val Pro Leu Ser Phe Phe Ser Pro Ser Gly
 305 310 315 320
 Pro Ala Pro Glu Ile Ser Pro Leu Glu Val Leu Asp Gly Asp Ser Lys
 325 330 335
 Ala Val Gln Leu Leu Leu Gln Lys Asp Ser Ala Pro Leu Pro Ser
 340 345 350
 Pro Ser Gly His Ser Gln Ala Ser Cys Phe Thr Asn Gln Gly Tyr Phe
 355 360 365
 Phe Phe His Leu Pro Asn Ala Leu Glu Ile Glu Ser Cys Gln Val Tyr
 370 375 380
 Phe Thr Tyr Asp Pro Cys Val Glu Glu Glu Val Glu Asp Gly Ser
 385 390 395 400
 Arg Leu Pro Glu Gly Ser Pro His Pro Pro Leu Leu Pro Leu Ala Gly
 405 410 415
 Glu Gln Asp Asp Tyr Cys Ala Phe Pro Pro Arg Asp Asp Leu Leu Leu
 420 425 430
 Phe Ser Pro Ser Leu Ser Thr Pro Asn Thr Ala Tyr Gly Gly Ser Arg
 435 440 445
 Ala Pro Glu Glu Arg Ser Pro Leu Ser Leu His Glu Gly Leu Pro Ser
 450 455 460
 Leu Ala Ser Arg Asp Leu Met Gly Leu Gln Arg Pro Leu Glu Arg Met
 465 470 475 480
 Pro Glu Gly Asp Gly Glu Gly Leu Ser Ala Asn Ser Ser Gly Glu Gln
 485 490 495
 Ala Ser Val Pro Glu Gly Asn Leu His Gly Gln Asp Gln Asp Arg Gly
 500 505 510
 Gln Gly Pro Ile Leu Thr Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln
 515 520 525
 Glu Leu Gln Ala Gln Asp Ser Val His Leu Ile
 530 535

<210> 7

<211> 522

<212> PRT

<213> Homo sapiens

<400> 7

Met Gly Leu Gly Arg Cys Ile Trp Glu Gly Trp Thr Leu Glu Ser Glu
 1 5 10 15
 Ala Leu Arg Arg Asp Met Gly Thr Trp Leu Leu Ala Cys Ile Cys Ile
 20 25 30
 Cys Thr Cys Val Cys Leu Gly Val Ser Val Thr Gly Glu Gly Gln Gly
 35 40 45
 Pro Arg Ser Arg Thr Phe Thr Cys Leu Thr Asn Asn Ile Leu Arg Ile
 50 55 60
 Asp Cys His Trp Ser Ala Pro Glu Leu Gly Gln Gly Ser Ser Pro Trp
 65 70 75 80
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Tyr Thr Gly Gln Trp Ser Glu Trp Ser Gln Pro Val Cys Phe Gln Ala
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<213> Mus musculus

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Gly Val Cys Arg Gly Val Ser Val Pro Glu Gln Gly Gly Gly Gly Gln
      35              40              45
Lys Ala Gly Ala Phe Thr Cys Leu Ser Asn Ser Ile Tyr Arg Ile Asp
      50              55              60
Cys His Trp Ser Ala Pro Glu Leu Gly Gln Glu Ser Arg Ala Trp Leu
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Leu Phe Thr Ser Asn Gln Val Thr Glu Ile Lys His Lys Cys Thr Phe

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 Cys Val Leu Thr Trp Gly Ile Asn Leu Ala Leu Glu Pro Leu Ile Thr
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 Lys Ser His Trp Ser Glu Trp Ser Gln Pro Val Ser Phe Pro Ser Pro
 245 250 255
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 Ile Leu Val Val Val Pro Ile Phe Leu Leu Leu Thr Gly Phe Val His
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 Ile Pro Ser Pro Glu Ala Phe Phe His Pro Leu Tyr Ser Val Tyr His
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 Gly Asp Phe Gln Ser Trp Thr Gly Ala Arg Arg Ala Gly Pro Gln Ala
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 Trp Glu Ala Val Ala Thr Leu Thr Tyr Ser Pro Ala Cys Pro Val Gln
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 Met Leu Asp Cys Cys Glu Glu Cys His Leu Ser Ala Phe Pro Gly His
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 Ser Ser Arg Ala
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/02

US CL : 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/198.1; 435/320.1, 325; 530/350; 536/23.1, 935/19, 23

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P — Y, P	US 6,057,128 A(DONALDSON et al.) 02 May 2000 (02.05.2000), see entire document, especially SEQ ID NO: 1 and 2.	1-9, 12, 13 4, 10
X, P — Y, P	LOFTUS et al. Genome duplications and other features in the 12 Mb of DNA sequence from human chromosome 16p and 16q. Genomics. 1999, Vol. 60, No. 3, pages 295-308, see sequence.	1, 2 3-7, 12, 13
X	HILLIER et al. Generation and analysis of 280,000 human expressed sequence tags. Genome Research. 1996, Vol. 9, pages 807-828, see AA129802.	1
Y	US 5,168,062 A (STINSKI) 01 December 1992 (01.12.1992), see column 10, lines 9-46.	3-7
Y	SCHMITT et al. Affinity purification of histidine-tagged proteins. Molecular Biology Reports. 1993, Vol. 18, pages 223-230, see entire document.	4, 10, 12

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

21 August 2000 (21.08.2000)

Date of mailing of the international search report

22 SEP 2000

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Ulrike Winkler, Ph.D.

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-10, 12 and 13

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-10, 12 and 13, drawn to a nucleic acid, a vector encoding nucleic acid, a polypeptide encoded by the nucleic acid and a method of producing the polypeptide using the nucleic acid..

Group II, claim(s) 11, drawn to an antibody.

Group III, claim(s) 14, 15 and 16, drawn to a method of detecting the presence of a polypeptide in a sample.

Group IV, claim(s) 17, 18 and 19, drawn to a method of detecting the nucleic acid.

Group V, claim(s) 20 and 21, drawn to a method of identifying compounds that bind the polypeptide.

Group VI, claim(s), 22 and 22, drawn to a method of modulating the activity of the polypeptide.

The inventions listed as group I-VI do not relate to a single general inventive concept under PCT rule 13.1 because, under unity of invention different categories of invention will only exist if specific combinations of inventions are present. Those combinations include:

A) A product and a special process of manufacture of said product.

B) A product and a process of use of said product.

C) A product, a special process of manufacture of said product and a process of use of said product.

D) A process and an apparatus specially designed to carry out said process.

E) A product, a special process of manufacture of said product, and an apparatus specially designed to carry out said process.

The allowed combinations do not include multiple products, multiple methods of using said products and a method of making a product as claimed in the instant application. Accordingly, groups I-VI are not so linked as to form a single general inventive concept.

Continuation of B. FIELDS SEARCHED Item 3: WEST 2.0, MEDLINE, GENE BANK,
SEQ ID NO: 1, 2, 3 and 4; interleukin receptor

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**INDICATIONS RELATING TO DEPOSITED MICROORGANISM
OR OTHER BIOLOGICAL MATERIAL**

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 4, line 2	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depository institution <p align="center">American Type Culture Collection</p>	
Address of depository institution (including postal code and country) <p align="center">10801 University Blvd. Manassas, VA 20110-2209 US</p>	
Date of deposit <p align="center">14 July 1999 (14.07.99)</p>	Accession Number <p align="center">PTA-350</p>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Page 13, line 14; page 17, line 31; page 20, line 4; page 23, line 32; page 28, line 24; page 90, lines 8,11,16,20,23 and 27; page 91, lines 3,7,25,28 and 32; page 92, lines 10,22,25,28 and 32; page 93, line 8	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indicators are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	
<input type="checkbox"/> This sheet was received with the international application	
Authorized officer	

For International Bureau use only	
<input type="checkbox"/> This sheet was received with the International Bureau on:	
Authorized officer	

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - 5 a) a nucleic acid molecule comprising a nucleotide sequence which is at least 45% identical to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof;
 - 10 b) a nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof;
 - 15 c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350;
 - 20 d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or the polypeptide encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350; and
 - 25 e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions.
- 30 2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

- a) a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, or a complement thereof; and
- b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.
3. The nucleic acid molecule of claim 1 further comprising vector nucleic acid sequences.
4. The nucleic acid molecule of claim 1 further comprising nucleic acid sequences encoding a heterologous polypeptide.
5. A host cell which contains the nucleic acid molecule of claim 1.
6. The host cell of claim 5 which is a mammalian host cell.
7. A nonhuman mammalian host cell containing the nucleic acid molecule of claim 1.
8. An isolated polypeptide selected from the group consisting of:
- (a) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350;
- b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the polypeptide is encoded by a nucleic acid molecule

which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions; and

- 5 c) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 45% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof.

9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

10. The polypeptide of claim 8 further comprising heterologous amino acid sequences.

15

11. An antibody which selectively binds to a polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

- 20 (a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

- 25 b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350; and

- 30 c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID

NO:3, or a complement thereof under stringent conditions; comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

5 13. The method of claim 12 wherein said polypeptide comprises the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number PTA-350.

10 14. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:
 a) contacting the sample with a compound which selectively binds to a polypeptide of claim 8; and
 b) determining whether the compound binds to the polypeptide in the
15 sample.

 15. The method of claim 14, wherein the compound which binds to the polypeptide is an antibody.

20 16. A kit comprising a compound which selectively binds to a polypeptide of claim 8 and instructions for use.

 17. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:
25 a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and
 b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample.

30 18. The method of claim 17, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

19. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 and instructions for use.

20. A method for identifying a compound which binds to a polypeptide of claim 8 comprising the steps of:

- a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and
- b) determining whether the polypeptide binds to the test compound.

21. The method of claim 20, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detecting of test compound/polypeptide binding;
- b) detection of binding using a competition binding assay;
- c) detection of binding using an assay for IL-9/IL-2 receptor-like-mediated signal transduction.

22. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

23. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

- a) contacting a polypeptide of claim 8 with a test compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

FIGURE 1

h16445 pro	MPR-----GMAAPL-----LGLLLGGGK-----GCPLVCYTDYLOVVICILEHMLNHP-ST 46
m16445 pro	MPR-----GPVAAAL-----LGLLLHGAAL-----SCDLCTCYDYLOVVICILEHMLNHP-ST 46
hIL-2 Rc beta pro	MNA-----PALSMRLPLLLILLPLATSN-----ASAVNGTSQPTCFYNSRANISCU-----WSQDQ-AL 54
mIL-2 Rc beta pro	MAT-----PALSMRLPLLLILLPLATSN-----ASAVNGTSQPTCFYNSRANISCU-----WSQDQ-AL 54
hIL-9 Rc pro	HGLORCIWZONTLESEVLRDDH-GTLLACICICTCVGVSTGECGQ-PRSRFTCTCLNNILRDC-----WSHEE-AL 54
mIL-9 Rc pro	MALORCIAEONTLESEVLRDDH-GTLLACICICTCVGVSTGECGQ-PRSRFTCTCLNNILRDC-----WSHEE-AL 54
h16445 pro	LALTLTWO-DQYBEELKDEZATSCSLHRSANAHATMAYTCHMDVPHF-----MADDFSVNIT-----DOSGNYSQECGSPLLA 116
m16445 pro	LALTLTWO-DQYBEELKDEZATSCSLHRSANAHATMAYTCHMDVPHF-----MADDFSVNIT-----DOSGNYSQECGSPLLA 116
hIL-2 Rc beta pro	QDTSQVHAMPPDRMMNQCCELLP-----VSOASMACNLLILGGA-PDSOKITTDIVTLRLV-CREGVWRVMAIODEKFFE 128
mIL-2 Rc beta pro	NVITICHUAKXSNLHWHNRTCELLP-----VSOASMACNLLILGGA-PDSOKITTDIVTLRLV-CREGVWRVMAIODEKFFE 128
hIL-9 Rc pro	GESPMWLLFTSNQAPQGTTHKICILRGSS-----ECTVVA-----PPEAVLVPSDNPTITFHHCMSREQVSLVDPEYLP 129
mIL-9 Rc pro	ESRAMLLFTSNQAPQGTTHKICILRGSS-----ECTVVA-----PPEAVLVPSDNPTITFHHCMSREQVSLVDPEYLP 129
h16445 pro	SIMPAPPFNVTVTFSG-----QYNISWRSDDYEDPAFYMLKQKLYELQYRNWQDPMAYSPRHKKLSVDSRSVSLPL-EP 192
m16445 pro	SIRPAPPFNVTVTFSG-----QYNISWRSDDYEDPAFYMLKQKLYELQYRNWQDPMAYSPRHKKLSVDSRSVSLPL-EP 192
hIL-2 Rc beta pro	NLRMLMAPISLQVHVHVEZHRCNISWELIS-QASHNFER-HLEFEARTLSPGHTEAP-----LTLKQKQEMICUE-TLTP 200
mIL-2 Rc beta pro	NLRMLMAPISLQVHVHVEZHRCNISWELIS-QASHNFER-HLEFEARTLSPGHTEAP-----LTLKQKQEMICUE-TLTP 200
hIL-9 Rc pro	HVKLDPPSDLO-SNISSGHCILTWSIS-----PALEPMITLUSYELAFKKQEEAVEQAQRHDIHG-----VTMLICEAFELDP 216
mIL-9 Rc pro	HIKLDPPSDLO-SNISSGHCILTWSIS-----PALEPMITLUSYELAFKKQEEAVEQAQRHDIHG-----VTMLICEAFELDP 216
h16445 pro	DSSYELQVRAO-----PMGSSVQGTWSEMSDPVIFOTOTSEELKEZ-----WNPMLLLLL-LLVIVYFIPA FWSLKT 257
m16445 pro	DSSYELQVRAO-----PMGSSVQGTWSEMSDPVIFOTOTSEELKEZ-----WNPMLLLLL-LLVIVYFIPA FWSLKT 257
hIL-2 Rc beta pro	DTQVEFOVRVK-----FLQGEF-----TTWSPWSOPLAERTKPAALQNDTIF-MGHLUGLGSAGAPFIILVYLLINC 267
mIL-2 Rc beta pro	STSYEVOVRVK-----FLQGEF-----TTWSPWSOPLAERTKPAALQNDTIF-MGHLUGLGSAGAPFIILVYLLINC 267
hIL-9 Rc pro	GFIHEARLRVOMATLE-DDDVLEERTTGWSEMSQPLVCFQAPOR-QGPLPEPMWPGNTLVAVSLELTOTVYLLFKL 270
mIL-9 Rc pro	GEIYEARLRVOM-TLESYEDKTEGEVYKSHMSEMSOPUSEPSPORRQGLVFRQMSASILVUVPTPELTLTGTFVHLLFKL 293
h16445 pro	HE-----LWRLWKKIWN-VPSPEPFHPLIKGCSGDFKRWGAPFTOSSLELGPWSPSEVPS-TLEVYSCHPPRSPAKRLQLT 332
m16445 pro	HL-----PWRLWKKIWN-VPSPEPFHPLIKGCSGDFKRWGAPFTOSSLELGPWSPSEVPS-TLEVYSCHPPRSPAKRLQLT 332
hIL-2 Rc beta pro	RNTGPM-LKKVLKCMTPDPSKPFSSOISEHGDDVOKMSSPSPSPSGGLAPESPLEVLEARD-KVTOGLLOQDNVPE 345
mIL-2 Rc beta pro	RYLGPW-LKTLVLECHIADPSZPFSSQSHQDLOKWLSEVLEPSPSPSGGLAPESPLEVLEARD-KVTOGLLOQDNVPE 345
hIL-9 Rc pro	SP-----RVNRIFYQNTSPSPAMFOPLYSVHNGMFTMGAHRAAGVLLSDCAGTPOGAL-PCVQENATLTCGPAPRPM 367
mIL-9 Rc pro	SP-----RLKRIFYQNTSPSPAMFOPLYSVHNGMFTMGAHRAAGVLLSDCAGTPOGAL-PCVQENATLTCGPAPRPM 367
h16445 pro	ELQZPAELVESDCGVPKESFW-----PTAONSGGSAYSEEDRPPYGLVSDITVTVDAREGCTWPCSCDDGYPALDL 409
m16445 pro	GLPLGLEEEQLECDGMSERPGHMCIIIPCAAGQAVSAYSEEDRPPYGLVSDITVTVDAREGCTWPCSCDDGYPALDL 409
hIL-2 Rc beta pro	PASLSNHSLSCTNCGYF-FPHLPDALEIEAC-----QVY-PTYDPYSEEDPDEGVAQAFSGEPOLPLSGEDDAY 418
mIL-2 Rc beta pro	PLPSPSGHSQNSCTNCGYF-FPHLPDALEIEAC-----QVY-PTYDPYSEEDPDEGVAQAFSGEPOLPLSGEDDAY 418
hIL-9 Rc pro	KSVALEEEEOGPGTRLPGN-----LSSEEDVLPACCTEMWVQTLAYLPQE-----DWAATSLTRPAPPSDEGSRSS 421
mIL-9 Rc pro	OFACLKWEATAPG-FPGCL-----PQSEHVLPAACCTEMWVQTLAYLPQE-----DWAATSLTRPAPPSDEGSRSS 421
h16445 pro	PSGLBEDPPLLDA GTTVLSGCVSAGSPGLGGLPGLSLLDRLKPPLA DGE-DMAOGLPMGGGRSPGGVSESEAGSPLA 487
m16445 pro	SGPNSEDLVLDPAFLSCGCVSGLRLGQSPSLDRLKPPLA DGE-DMAOGLPMGGGRSPGGVSESEAGSPLA 487
hIL-2 Rc beta pro	CTPSPSRDLDLLFSPSLI-GOPSPSTAPQSGAGE-EMPPSLQERVPRMDPO-PLGPTTPGVDDLVDFOPPELVLR 494
mIL-2 Rc beta pro	CAPPSPRDLDLLFSPSLI-GOPSPSTAPQSGAGE-EMPPSLQERVPRMDPO-PLGPTTPGVDDLVDFOPPELVLR 494
hIL-9 Rc pro	SSSSESSN-NNNYCALGCG-----STPNTAYGGSRAPE-ERSPLSHE-----GLPSLASRDLMLGLQRP 482
mIL-9 Rc pro	SSSSESSN-NNNYCALGCG-----STPNTAYGGSRAPE-ERSPLSHE-----GLPSLASRDLMLGLQRP 482
h16445 pro	DFDGSOFVGSDCSPVECDFTSPGDEGPPRSYLROWVVI PPP-----LESPPGQAS- 539
m16445 pro	DFDGSOFVGSDCSPVECDFTSPGDEGPPRSYLROWVVI PPP-----LESPPGQAS- 539
hIL-2 Rc beta pro	EA-GEV PDA GPREGVSTFWEPPGQGFALNARLPNTDAYLSLOELQGDPTHLV 530
mIL-2 Rc beta pro	GD-GEGLSANSSEZQASVEGNLHGQDQDQGPILTLNTDAYLSLOELQGDPTHLV 530
hIL-9 Rc pro	G-LSCDHQQLETQGVAVVLAGHCORPOLHEDLOHLLPVS-----LSKARSMTF- 533
mIL-9 Rc pro	G-LSCDHQQLETQGVAVVLAGHCORPOLHEDLOHLLPVS-----LSKARSMTF- 533

Decoration '1': Shade (with solid black) residues that match the Consensus exactly.

FIGURE 2

h 16445 Expression

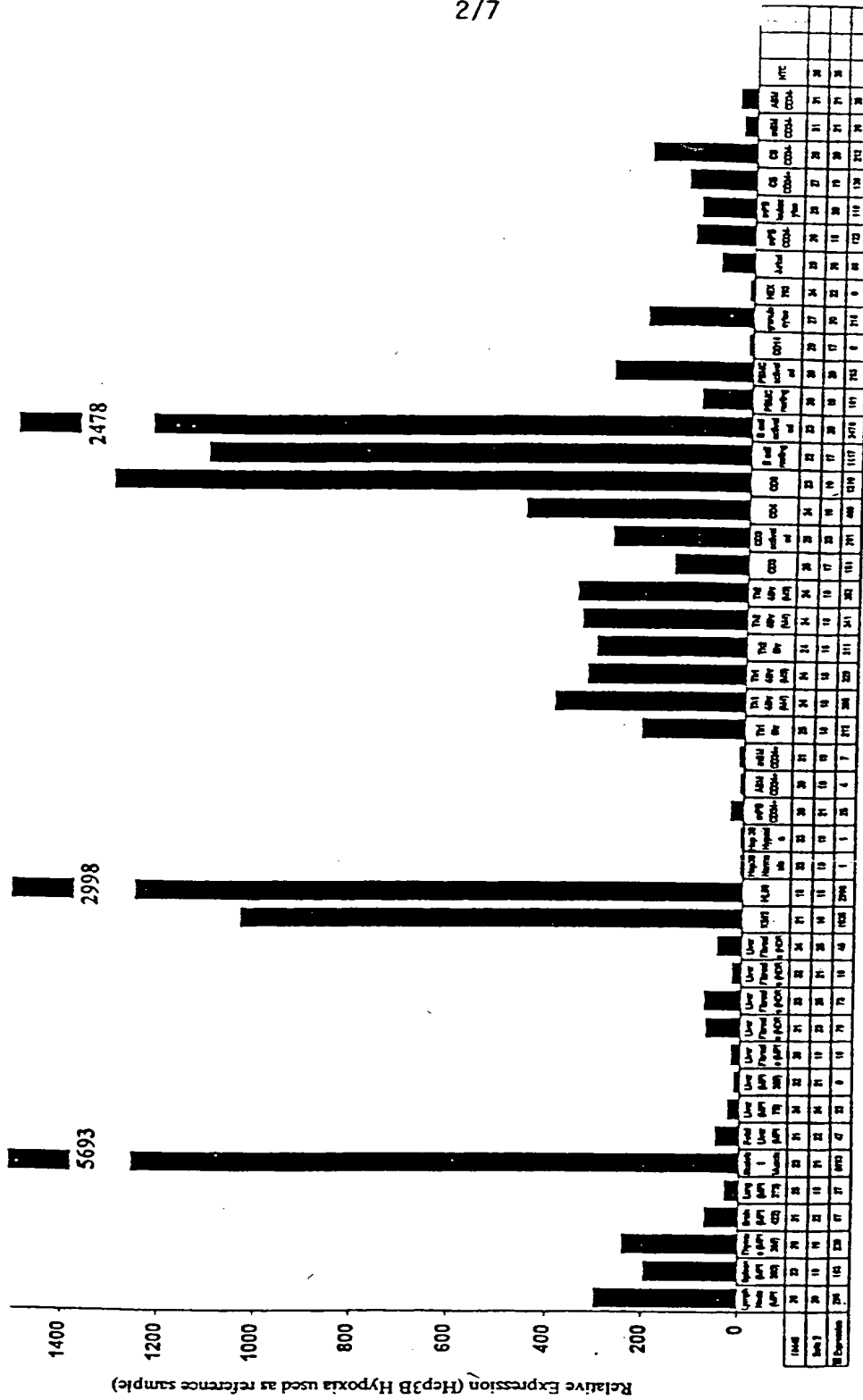


FIGURE 3A

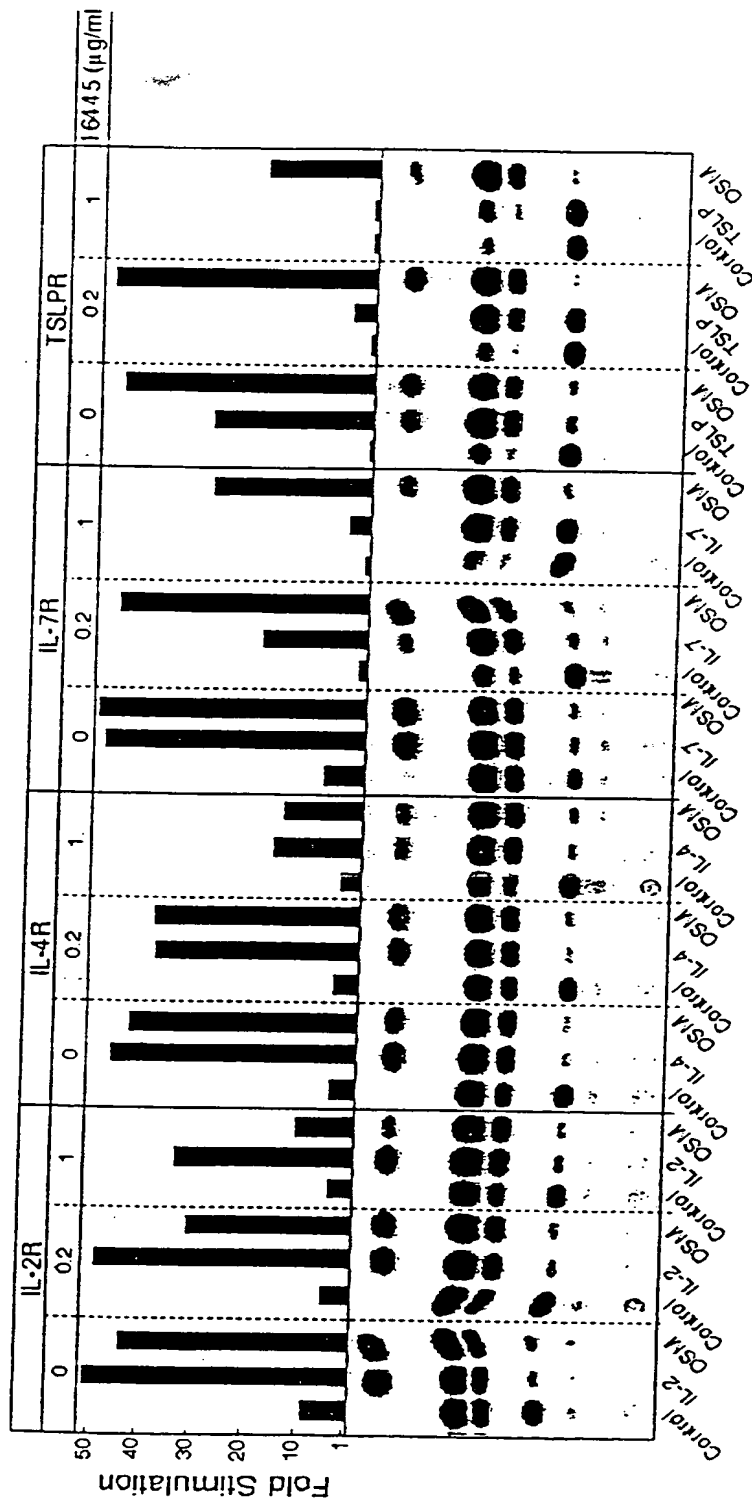


FIGURE 3B

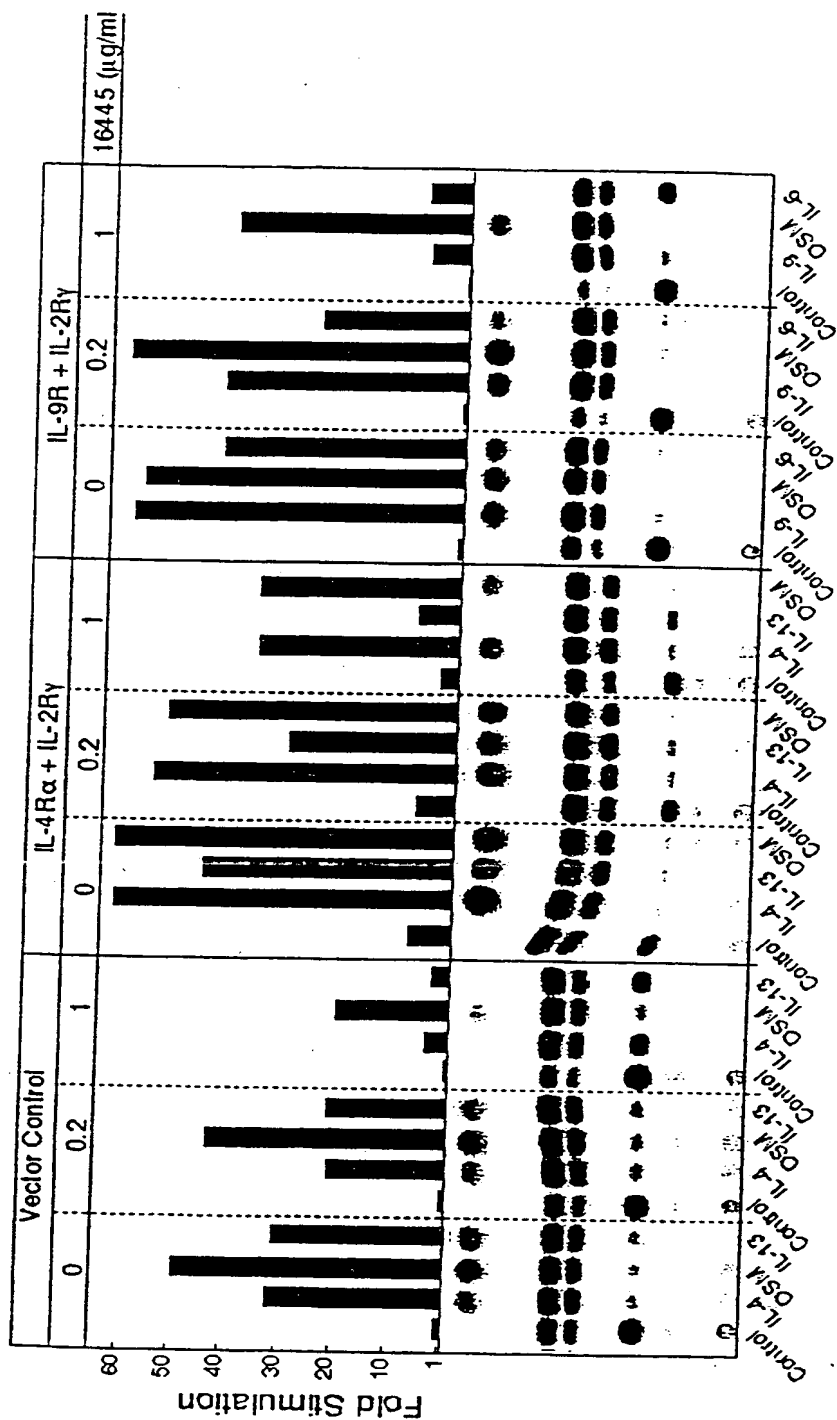


FIGURE 4

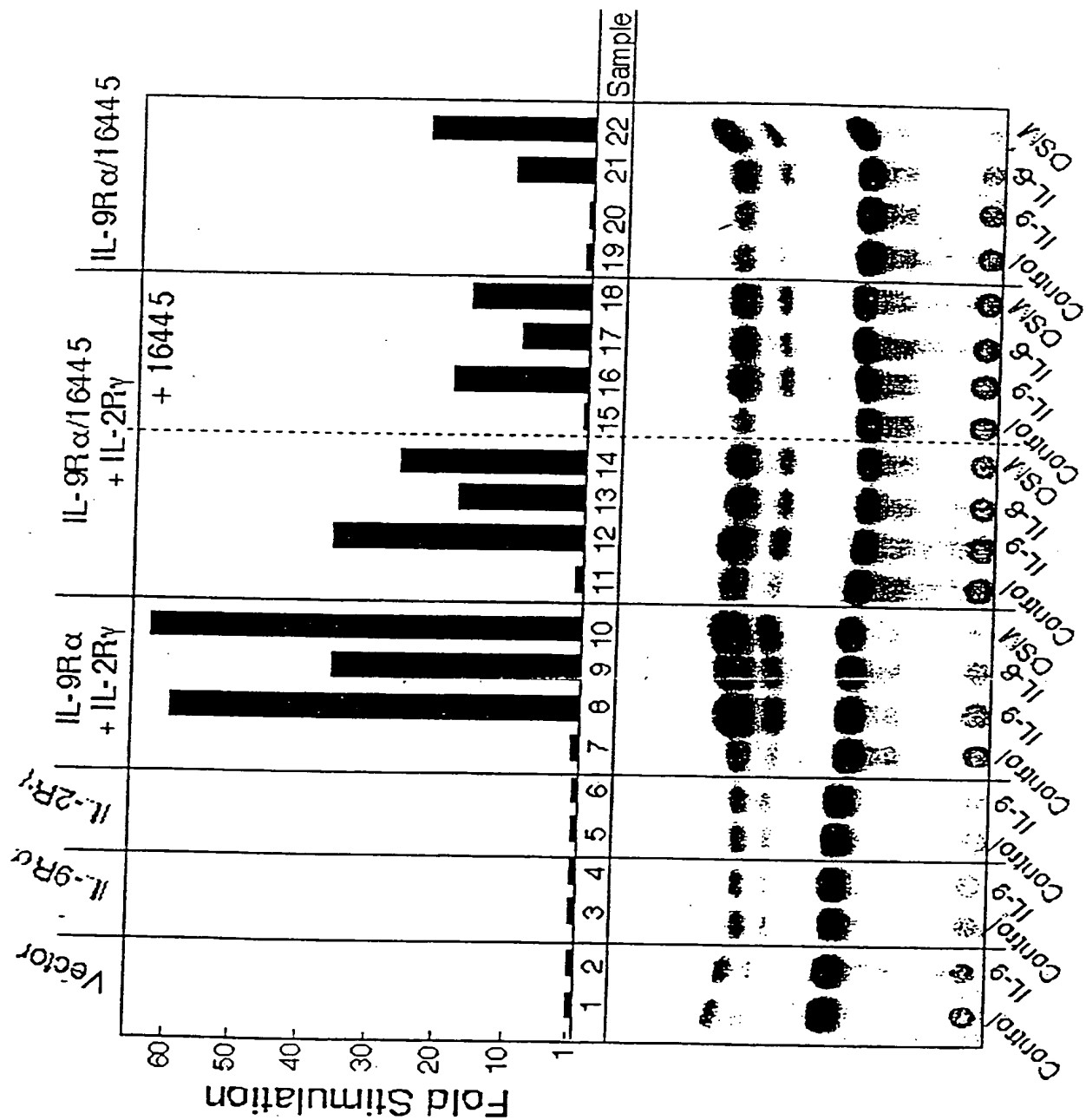


FIGURE 5

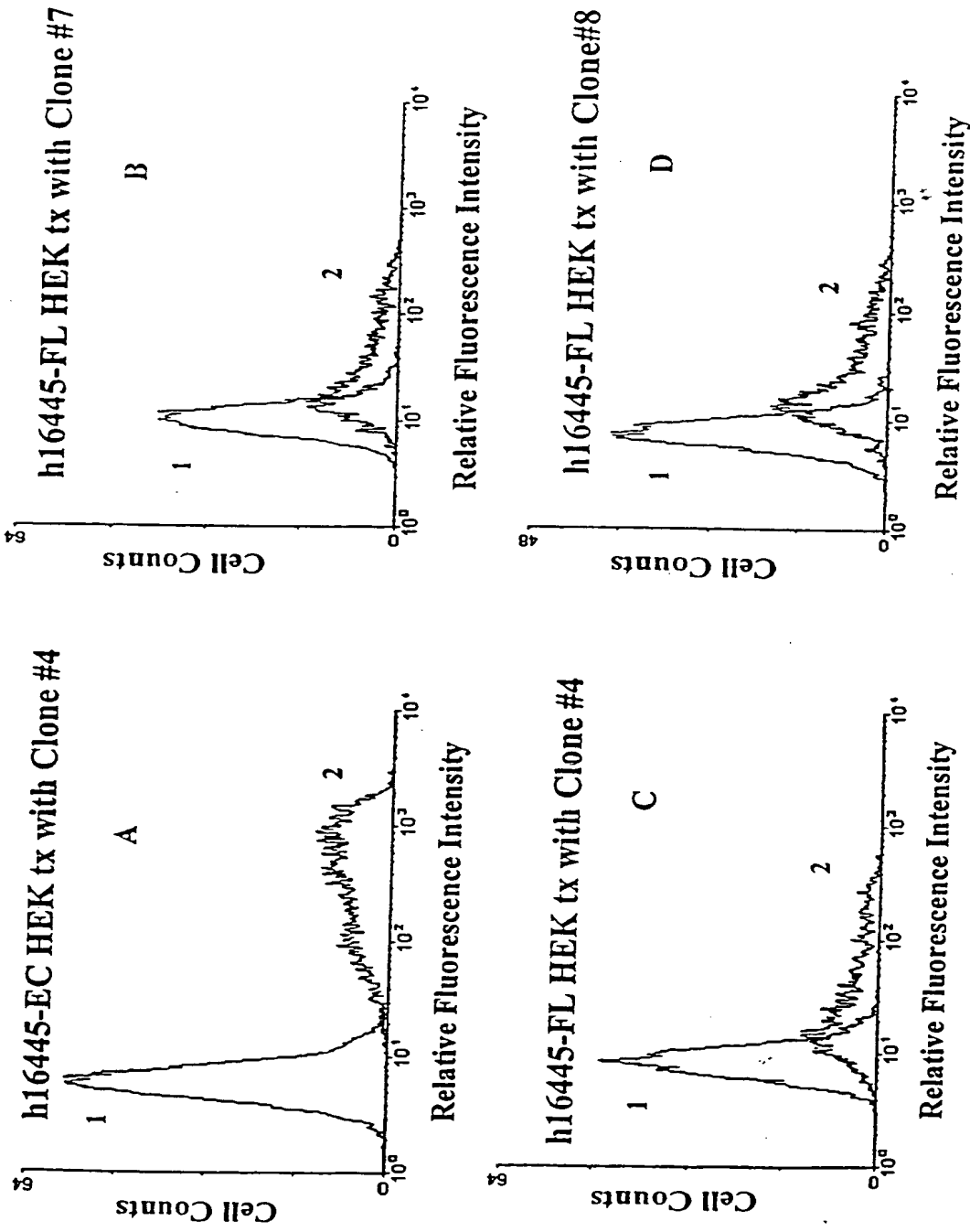
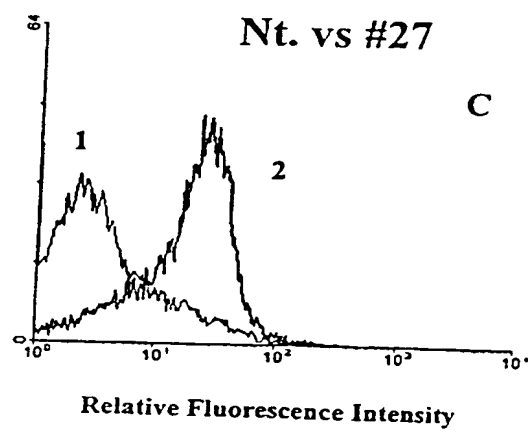
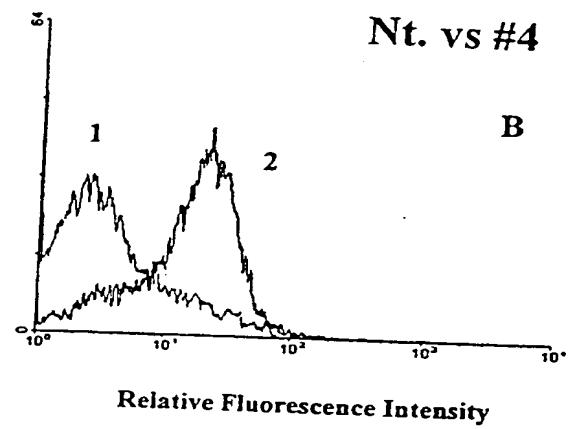
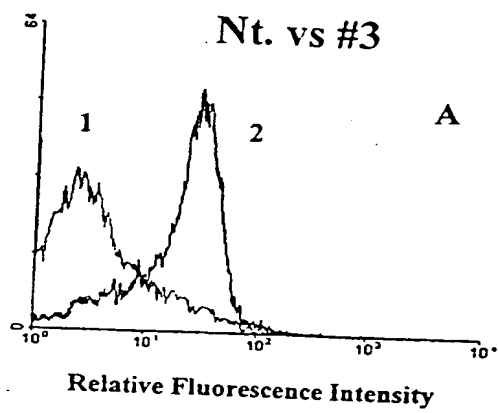


FIGURE 6



SEQUENCE LISTING

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and Uses Thereof

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<151> 1999-05-18

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tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc      453
Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
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Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
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caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc      549
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His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
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gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca      645
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Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser	
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Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe	
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tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg	837
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg	
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Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp	
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Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser	
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Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln	
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Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser	
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gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctg ctg ctg	1077
Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu Leu	
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ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat cca	1125
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Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu Arg	
260 265 270 275	
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Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp Ser	
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Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro Arg	
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agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca gag	1365
Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala Glu	
325 330 335	
ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca gcc	1413
Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr Ala	

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Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr	360	365	370	
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Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro	375	380	385	
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Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp	390	395	400	
ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg				1605
Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu	405	410	415	
gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc agc				1653
Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser	420	425	430	435
cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca				1701
Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro	440	445	450	
ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc				1749
Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly	455	460	465	
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Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu Ala	470	475	480	
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Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys	485	490	495	
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Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro	500	505	510	515
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Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser	520	525	530	
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Ser Pro Gly Pro Gln Ala Ser	535			
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Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
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Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
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210 215 220
Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
225 230 235 240
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Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
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Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala	
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Lys Ile Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu	
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Tyr Arg Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe	
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Ala Leu His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly	
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 Cys Ser Leu His Lys Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
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 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
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 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/02
US CL : 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 424/198.1; 435/320.1, 325; 530/350; 536/23.1, 935/19, 23

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P — Y, P	US 6,057,128 A(DONALDSON et al.) 02 May 2000 (02.05.2000), see entire document, especially SEQ ID NO: 1 and 2.	1-9, 12, 13
X, P — Y, P	LOFTUS et al. Genome duplications and other features in the 12 Mb of DNA sequence from human chromosome 16p and 16q. Genomics. 1999, Vol. 60, No. 3, pages 295-308, see sequence.	4, 10 1, 2
X Y Y	HILLIER et al. Generation and analysis of 280,000 human expressed sequence tags. Genome Research. 1996, Vol. 9, pages 807-828, see AA129802. US 5,168,062 A (STINSKI) 01 December 1992 (01.12.1992), see column 10, lines 9-46. SCHMITT et al. Affinity purification of histidine-tagged proteins. Molecular Biology Reports. 1993, Vol. 18, pages 223-230, see entire document.	3-7, 12, 13 1 3-7 4, 10, 12

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

Special categories of cited documents:

- * "A" document defining the general state of the art which is not considered to be of particular relevance
- * "E" earlier application or patent published on or after the international filing date
- * "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- * "O" document referring to an oral disclosure, use, exhibition or other means
- * "P" document published prior to the international filing date but later than the priority date claimed

"T"

later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

21 August 2000 (21.08.2000)

Date of mailing of the international search report

22 SEP 2000

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Ulrike Winkler, Ph.D.

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-10, 12 and 13

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/13687

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-10, 12 and 13, drawn to a nucleic acid, a vector encoding nucleic acid, a polypeptide encoded by the nucleic acid and a method of producing the polypeptide using the nucleic acid..

Group II, claim(s) 11, drawn to an antibody.

Group III, claim(s) 14, 15 and 16, drawn to a method of detecting the presence of a polypeptide in a sample.

Group IV, claim(s) 17, 18 and 19, drawn to a method of detecting the nucleic acid.

Group V, claim(s) 20 and 21, drawn to a method of identifying compounds that bind the polypeptide.

Group VI, claim(s), 22 and 22, drawn to a method of modulating the activity of the polypeptide.

The inventions listed as group I-VI do not relate to a single general inventive concept under PCT rule 13.1 because, under unity of invention different categories of invention will only exist if specific combinations of inventions are present. Those combinations include:

A) A product and a special process of manufacture of said product.

B) A product and a process of use of said product.

C) A product, a special process of manufacture of said product and a process of use of said product.

D) A process and an apparatus specially designed to carry out said process.

E) A product, a special process of manufacture of said product, and an apparatus specially designed to carry out said process.

The allowed combinations do not include multiple products, multiple methods of using said products and a method of making a product as claimed in the instant application. Accordingly, groups I-VI are not so linked as to form a single general inventive concept.

Continuation of B. **FIELDS SEARCHED** Item 3: WEST 2.0, MEDLINE, GENE BANK,
SEQ ID NO: 1, 2, 3 and 4; interleukin receptor

BEST AVAILABLE COPY